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(54) Title: OLFACTORY RECEPTOR SEQUENCES

(57) Abstract: The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensation. The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these polynucleotide sequences and host cells transfected with these polynucleotide sequences. The present invention further provides for functional variants and homologues of these polynucleotide sequences and the polypeptides encoded by these polynucleotides. Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of polypeptides in screening odorant molecules to determine the correspondence (scent representation, scent fingerprint or scent profile) between individual odorant receptors (the polypeptides) and particular odorant molecules. Also encompassed by the present invention is the use of the scent representation, scent fingerprint or scent profile to re-create and edit scents.

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OLFACTORY RECEPTOR SEQUENCES

CROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims priority benefit of United States Provisional Patent Application Serial No. 60/158,615, filed on October 8, 1999, and United States Provisional Patent Application Serial No. 60/184,809, filed on February 24, 2000. The contents of those applications are hereby incorporated by reference herein in their entirety.

STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH

Not applicable.

TECHNICAL FIELD

15 The present invention is in the field of human olfactory receptors and their use in screening for olfactory agonists and antagonists. The present invention pertains to isolated nucleotide sequences which encode human olfactory receptors and also to the proteins
20 encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of secondary scents and the identification of
25 combinations of odor receptors which are encoded to detect such secondary scents.

BACKGROUND ART

Our sense of smell plays an important role not only in our appreciation of our surroundings such as the smell of flowers or new mown grass, but also evolved as a survival skill. Numerous odorant molecules can be detected at extremely low concentrations, providing early warning of danger, such as the smell of smoke or contaminated food. Indeed, a potent example of this is that most pregnant women experience a heightened sense of smell, presumably to protect the fetus from the deleterious effects of food poisoning.

It is estimated that humans can detect millions of different molecular species; however, our nose can discriminate only a fraction of these different chemicals (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320), usually estimated at about 10,000 odorants (Axel, *Scientific American* 1995, October, 154-159). Odorants for terrestrial species such as humans, are volatile (air born) ligands which are detected by the olfactory system. Odorants have vastly different chemical structures and subtle differences can lead to pronounced changes in the perceived odor (Mombaerts, *supra*). For instance, when the hydroxyl group of octanol is replaced by a carboxyl group to give octanoic acid, its perceived odor changes from orange and rose-like to rancid and sweaty (Malnic *et al.*, *Cell* 1999 96, 713-723). The basis for these feats of sensory perception are just beginning to be understood at a cellular and molecular level.

The olfactory system contains millions of olfactory sensory neurons (OSNs) located in the olfactory epithelium of the nasal cavity. In humans, the olfactory epithelium occupies an area of approximately 5 cm². The OSNs are bipolar with one end extending through the supporting cell into the mucosal layer, terminating in hairlike cilia. These cilia are the site of the olfactory receptors (OR) where the odorant ligands are thought to bind (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320, Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). The OSNs also have a single unbranched axon which leads to the olfactory bulb, a part of the brain containing approximately 2000 glomeruli where the axons terminate and initial processing of the sensory code takes place. OSNs expressing the same OR are randomly interspersed throughout the olfactory epithelium, but in both the nose and the bulb, information derived from different ORs is strictly segregated; each OSN in the nose and each glomerulus in the olfactory bulb appear to be dedicated to input from one or few OR type(s) (Malnic *et al.*, *Cell* 1999 96, 713-723). It also appears that the location of the glomeruli are conserved across individuals of a species, providing the first spatial processing of particular odorant patterns (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). The domains in the olfactory bulb for

different odors may overlap, but the overall patterns are distinct (Hildebrand *et al.*, *supra*), therefore, it should be possible to identify and reproduce the characteristic pattern of a given odorant. Output neurons project from the olfactory bulb to the primary olfactory cortex and from there to the higher cortical areas of the brain and to the limbic system (Malnic *et al.*,
5 *supra*; Hildebrand *et al.*, *supra*, 20, 595-631).

Until the identification of a large family of genes encoding putative odorant receptors (Buck & Axel *Cell* 1991 65, 175-187), progress towards understanding the process of odor recognition was negligible. In recent years there has been an explosion in this field as more and more putative odor receptors are isolated and cloned. The odorant receptor gene products
10 have thus far been characterized through homology as seven transmembrane domain G protein-coupled receptors (GPCR). It is estimated that there are probably 500-750 OR-like sequences in humans, while there are 500-1000 OR genes in rat and mouse (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). In mice, OR-like sequences make up approximately 1% of their genome, the largest known family in the mammalian genome, surpassing the complexity of
15 even the immunoglobulin and T-cell antigen receptor gene families (Mombaerts, *supra*). The OR are concentrated on the surface of the OSN's mucus coated cilia and it is thought that odorant molecules bind to the OR in the olfactory epithelium and thereby initiate signal transduction. Current interpretation of recent experimental evidence favors the idea that each neuron expresses only one, or very few, ORs. Since mammals can detect at least 10,000 odors and
20 there are approximately 1,000 or fewer ORs, each of the ORs must respond to several odorant molecules, and each odorant molecule must bind to several receptors. It is believed that various receptors respond to discrete parts of an odorant molecule's structure and that an odorant consists of several chemical groups each of which bind a characteristic receptor (Axel
Scientific American 1995, October, 154-159; Malnic *et al.*, *Cell* 1999 96, 713-723).

25 The main signal transduction pathway mediated by OR homologues in vertebrate species involves G protein-mediated stimulation of adenylyl cyclase activity, resulting in cAMP elevation that opens cyclic-nucleotide gated channels with a non-specific cation selectivity (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). However, there are still numerous unanswered questions and recently it has come to light that 38-76% of the human
30 gene OR sequences that are being reported may be pseudogenes and therefore incapable of expressing the proteins that encode the olfactory receptors. Some of the incidences may be due to the method of extracting the genomic DNA libraries (Mombaerts, *supra*). Few pseudogenes have been found in other vertebrates and their incidence in libraries from testicular DNA is also

rare (Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). cDNA should not contain pseudogenes. There are a number of examples of ORs which have been successfully expressed and reactions to certain odorant ligands have been determined (Malnic *et al.*, *Cell* 1999 96, 713-723; Mombaerts, *supra*; Zhao *et al.*, *Science* 1998 279, 237-242).

5 Some attempts to express the ORs in heterologous cell lines resulted in the formation of inclusion bodies rather than the insertion of the proteins into the membrane (Kiefer *et al.*, *infra*). However, purification of the receptors after expression in *E. coli* and their insertion into lipid vesicles facilitates the use of these receptors in odorant ligand screening using a combination of photoaffinity labeling and Trp fluorescence (Kiefer *et al.*, *Biochemistry* 1996
10 35, 16077-16084). In addition, a functional human OR receptor protein has been expressed in HEK-293 cells and oocytes and found to interact with odorant ligands (Wetzel *et al.*, *J. Neurosci.* 1999 19, 7426-7433). There have also been, a number of successful efforts of expressing cDNA in insect Sf9 cells using *baculovirus* vectors (Mombaerts *Annu. Rev. Neuosci.* 1999) as well as assays with neuronal tissue (Malnic *et al.*, *Cell* 1999 96, 713-723;
15 Zhao *et al.*, 1998; Firestein *et al.*, WO 98/50081). In addition, recent work accomplished the expression of chimeric mouse olfactory receptor sequences in HEK-293 cells and showed their reactivity towards a panel of odorant ligands, some at micromolar concentrations (Krautwurst *et al.*, *Cell* 1998 95 917-926). The drawback to expression in heterologous cell systems is the lack of working signal transduction pathways which can be used to detect responses to odorant
20 ligands; these drawbacks can be overcome with methods known in the art (e. g. U.S. Pat. No. 5,798, 275). There are also methods of expressing and assaying functional neuronal receptors in neuronal cells, including methods for detecting particular odorant ligand specificity (Malnic *et al.*, *supra*; Zhao, *supra*; Firestein *et al.*, *supra*).

25 Other publications of interest are: *Chemical Senses* 6: 343-349 (1981); *Proc. Natl. Acad. Sci. USA* 79: 670-674 (1982); *Proc. Natl. Acad. Sci. USA* 81(6): 1859-1863 (1984); *Nature* 316: 255-258 (1985); *Brain Research* 368: 329-338 (1986); *J. Biol. Chem.* 261: 1299-1305 (1986); *Proc. Natl. Acad. Sci. USA* 83(13): 4947-4951 (1986); *J. Neurosci.* 6: 2146-2154 (1986); *J. Neurochem.* 47: 1527-1533 (1986); *Chemical Senses* 13: 191-204
30 (1988); *Biochem. J.* 260:121-126 (1989); *J. Biol. Chem.* 264: 6780-6785 (1989); *Biochim. Biophys. Acta* 1013: 68-72 (1989); *J. Biol. Chem.* 264: 18803-18807 (1989); *Biochemistry* 29: 7433-7440 (1990); *FEBS Lett.* 270: 24-29 (1990); *Chemical Senses* 15: 529-536 (1990); *Eur. J. Biochem.* 196: 51-58 (1991); *Nature* 349: 790-793 (1991); *Neurosci. Lett.* 141: 115-

118 (1992); Developmental Brain Res. 73: 7-16 (1993); Proc. Natl. Acad. Sci., USA 90: 3715-3719 (1993); Human Mol. Genetics 3: 229-235 (1994); Eur. J. Biochem. 225: 1157-1168 (1994); European Journal of Biochemistry 238: 28-37 (1996); Receptors and Channels 4: 141-147 (1996); Genomics 37(2): 147-160 (1996); Protein Science 8: 969-977 (1999); Genomics 53: 56-68 (1998); Genomics 61:24-36 (1999); Genomics 63: 227-245 (2000); Trends in Neurosci. 7:35-36 (1984); Ann. Rev. Neurosci. 9:329-355 (1986); Trends Biochem. Sci. 12:63-66 (1987); Nature 351: 275-276 (1991); Nature 353: 799-800 (1991); Current Biol. 3(10): 668-674 (1993); Nature 372:321-322 (1994); Essays in Biochemistry. 33: 93-104 (1998); and Nature, 398 (6725): 285-287 (1999).

10 However, despite the forgoing, there has been relatively little work with human olfactory receptors, in particular in determining the sequences of large numbers of receptors, and less progress in determining the correspondence between particular human olfactory receptors and the scent(s) to which they respond.

15 All publications cited herein are hereby incorporated by reference in their entirety.

DISCLOSURE OF THE INVENTION

20 An object of the invention is to determine the correspondence between ORs and the scent(s) to which they respond. Once this is accomplished, scents can be both analyzed and re-created for enhancing human experiences or eliciting particular responses. The present invention pertains to isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation. The present invention also pertains to the proteins encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the

25 nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of receptor complex scent components and the identification of combinations of odor receptors which are encoded to detect such receptor complex scent

30 components scents.

The invention provides isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation that are isolated from human olfactory epithelial tissue. The invention further provides expression vectors containing such nucleotide sequences. Also provided by the invention are purified polypeptides encoded by the nucleotide sequences. The invention further provides transformed cells which comprise a suitable host cell transfected with a suitable expression vector containing the nucleotide sequence encoding the receptor. The present invention also encompasses nucleotide sequences isolated from human olfactory epithelial tissue which encode receptors capable of binding odorant molecules. The invention further provides expression vectors containing such nucleotide sequences and homologues of both the polynucleotides and polypeptides. Further, the invention provides a means of using the nucleotide sequences of the invention in a method of screening odorant ligands to determine the specific binding of odorant molecules to a particular receptors, and further, determining the component odorant molecules of subjectively experienced smells, determining the combination odorant molecules and receptor stimulation or inhibition to re-create a particular scent. The binding of odorant molecules by the receptors encompassed in the present invention includes binding resulting in both the agonism (excitation/activation) and antagonism (inhibition/blocking) of receptor function(s) upon binding of the molecule.

Accordingly, the invention includes an isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence at least 95% homologous to said sequences. The invention also encompasses the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention. The invention further encompasses fragments of said polynucleotides which can be used as probes or primers to identify additional polynucleotide sequences through techniques known in the art, including those fragments depicted in SEQ ID NOs: 74-105.

The invention also includes additional isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides

encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:153 through SEQ ID NO: 1084, or a nucleotide sequence at least 95% homologous to said sequences. The invention also comprises the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

The invention also encompasses an isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function. Host cells expressing such polypeptides and phages displaying such polypeptides are also encompassed by the invention. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

Scents can be captured, analyzed and recorded by a sensory device using various methods. Scent capture can be initiated by the user or by an automatic sensing system. A scent can be analyzed in terms of its interaction with olfactory neurons of a mammalian, preferably human, olfactory system, or by the expression of individual receptors under appropriate conditions and appropriate assay conditions in multiwell plates or in terms of its perception by a panel of mammalian, preferably human, subjects. The interaction with olfactory neurons can be determined experimentally, in vitro, by determining the interaction of an odorant with olfactory receptors of a given type. Alternatively, the interaction with olfactory receptor can be determined using a computer simulation which provides information regarding the interaction of an odorant with the olfactory receptors. A panel of subjects can be used to represent odors in terms of their perception. The data so generated can be used to represent a scent in a manner which can be recorded in digital or other format, stored in media such as computer memory, disks, or printed format, and transmitted over a data network. The representation of the scent can be used to re-create the scent at a local or remote site using an emitter module. The

representation of the scent allows for scent editing, where desirable aspects of an odor are enhanced or added and undesirable aspects are attenuated or eliminated.

Accordingly, the invention also embraces libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084, where the polynucleotides encode functional olfactory receptors; or functional fragments of the expression products. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

Also encompassed by the invention are libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, where the polypeptides are functional olfactory receptors; or functional fragments of the polypeptides. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

The invention also embraces methods for determining the binding pattern of a composition with olfactory receptors, involving exposing the composition to an olfactory receptor library, and determining whether the composition binds to each olfactory receptor, thereby determining the overall binding pattern of the composition. In additional embodiments, the method also involves determining the approximate binding constant with which the composition, or the various chemicals within the composition, bind to the receptors; determining whether a receptor or functional fragment thereof is activated; and determining the absolute amount of activation, or amount of activation relative to another receptor or a control substance. The composition can consist essentially of one compound or chemical, or can comprise at least two compounds or chemicals.

The invention also embraces DNA arrays or DNA chips comprising the DNA segments derived from any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084. The invention also embraces a method of determining differences among one or more individuals with respect to their olfactory faculties, comprising the steps of comparing the olfactory DNA of each individual against the array or chip.

The invention also embraces a method to determine single nucleotide polymorphisms in olfactory receptors, comprising the steps of uniquely amplifying olfactory receptor sequences from DNA obtained from one or more individuals, based on

primers designed according to the first 25 bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084, and determining the similarities and differences between said amplified DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

5

Brief Description of the Drawings

Figure 1 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 1 - 73.

Figure 2 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 111 - 152.

Detailed Description of the Invention

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The present invention provides isolated polynucleotides comprising sequences that encode polypeptides which are involved in olfactory sensation and which can be used to screen odorant ligands, *e.g.*, odorant receptor agonists and antagonists.

Definitions

The term "olfactory receptor" (OR) refers to a polypeptide involved in olfactory sensation. An "olfactory receptor polynucleotide" or "OR polynucleotide" is a polynucleotide encoding a polypeptide involved in olfactory sensation.

The term "odorant ligand" as employed herein refers to a molecule that has the potential to bind to an olfactory receptor. Equivalent terms employed herein include "odorant", "odorant molecule" and "odorant compound". The term "binding" or "interaction" as used herein with respect to odorant ligands refers to the interaction of ligands with the receptor polypeptide where the ligands may serve as either agonists and/or antagonists of a given receptor or receptor function. An odorant ligand may thus directly cause a perception of odor (an agonist), or may block the perception of odor (an antagonist). An odorant ligand may include, but is not limited to, molecules which interact with polypeptides involved in olfactory

sensation. Odorant ligands and molecules which interact with olfactory receptors are generally small, approximately 1000 Daltons, more preferably approximately 750 Daltons, more preferably approximately 500 Daltons, or even more preferably approximately 300 Daltons, hydrophobic molecules with a variety of functional groups. Small changes in structure can induce profound changes in odorant ligand binding and hence in the odor perceived by an individual.

A more detailed description of these sequences, as well as how these sequences were obtained, is provided below.

10

As used herein, a "polynucleotide" is a polymeric form of nucleotides of any length, which contain deoxyribonucleotides, ribonucleotides, and/or their analogs. The terms "polynucleotide", "nucleotide" and "nucleic acid" as used herein are used interchangeably. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The term "polynucleotide" includes double-, single-stranded, and triple-helical molecules. Unless otherwise specified or required, any embodiment of the invention described herein that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double stranded form. Not all linkages in a polynucleotide need be identical.

20

The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, primers, and adaptors. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. The use of uracil as a substitute for thymine in a deoxyribonucleic acid is also considered an analogous form of pyrimidine.

25

In the context of polynucleotides, a "linear sequence" or a "sequence" is an order of nucleotides in a polynucleotide in a 5' to 3' direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polynucleotide. A "partial sequence" is a linear sequence of part of a polynucleotide which is known to comprise additional residues in one or both directions.

30

If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by

conjugation with a labeling component. Other types of modifications included in this definition are, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, cabamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., α -anomeric nucleic acids, peptide nucleic acids, etc.), as well as unmodified forms of the polynucleotide(s).

Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH groups can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups.

Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, but not limited to, 2'-O-methyl-, 2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carboxycyclic sugar analogs, α -anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs and abasic nucleoside analogs such as methyl riboside.

Although conventional sugars and bases will be used in applying the method of the invention, substitution of analogous forms of sugars, purines and pyrimidines can be advantageous in designing a final product, as can alternative backbone structures like a polyamide backbone such as those used in peptide nucleic acids (PNAs).

A polynucleotide or polynucleotide region has a certain percentage (for example, 75%, 80%, 85%, 90%, 95% or 99%) of "sequence identity" to another sequence means that, when aligned, that percentage of bases are the same in comparing the two sequences.

Homology, as described herein, means that the polypeptide sequences that are encoded by the nucleic acids demonstrate a certain relatedness (i.e., there exists regions of conserved amino acids), but not the same amino acid identity. There is complete or 100% homology at a particular amino acid residue when the amino acids of sequences being compared are the same (there is identity) or represent a conservative amino acid substitution (there is homology). A

"conservative amino acid substitution" occurs when a particular amino acid is substituted by an alternate amino acid of similar charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Ile). A "nonconservative amino acid substitution" occurs when a particular amino acid is substituted by an alternative amino acid of differing properties, that is, charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Tyr). The nucleic acid sequences within the scope of the present invention include those nucleic acids which differ in exact sequence from those listed in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152 but which encode identical or homologous polypeptide amino acid sequences.

A "primer" is a short polynucleotide, generally with a free 3' -OH group, that binds to a target potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target.

An "adaptor" is a short, partially-duplexed polynucleotide that has a blunt, double-stranded end and a protruding, single-stranded end. It can be ligated, through its double-stranded end, to the double-stranded end of another polynucleotide. This provides known sequences at the ends of thus modified polynucleotides. Often adaptors contain specific sequences for primer binding and/or restriction endonuclease digestion.

A "probe" when used in the context of polynucleotide manipulation refers to a polynucleotide which is provided as a reagent to detect a target potentially present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and enzymes.

"Transformation" or "transfection" refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, lipofection, transduction, infection or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host cell genome.

A polynucleotide is said to "encode" a polypeptide if, in its native state or when manipulated by methods well known to those skilled in the art, it can be transcribed and/or translated to produce the polypeptide, a homologous polypeptide or a fragment thereof. For purposes of this invention, and to avoid cumbersome referrals to complementary strands, the anti-sense (or complementary) strand of such a polynucleotide is also said to encode the

sequence; that is, a polynucleotide sequence that "encodes" a polypeptide includes both the conventional coding strand and the complementary sequence (or strand).

The terms "polypeptide", "oligopeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, it may be interrupted by non-amino acids, and it may be assembled into a complex of more than one polypeptide chain. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), as well as other modifications known in the art.

In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an N-terminal to C-terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide. A "partial sequence" is a linear sequence of part of a polypeptide which is known to comprise additional residues in one or both directions.

"Recombinant," as applied to a polynucleotide or gene, means that the polynucleotide is the product of various combinations of cloning, restriction and/or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature.

A "vector" is a self-replicating nucleic acid molecule that can be used to transfer an inserted nucleic acid molecule into and/or between host cells. The term includes vectors that function primarily for insertion of a nucleic acid molecule into a cell, vectors that function primarily for the amplification of nucleic acid, and expression vectors that function for transcription and/or translation of the DNA or RNA. Also included are vectors that provide more than one of the above functions.

"Expression vectors" are defined as polynucleotides which, when introduced into an appropriate host cell, can be transcribed into a mRNA capable of being translated into a polypeptide(s). An expression vector also comprises control elements operatively linked to the coding region to enable and/or facilitate expression of the polypeptide in the target cell. These can include transcriptional, translational, posttranscriptional, and posttranslational control elements, as are known in the art. An "expression system" usually connotes a suitable host cell comprised of an expression vector that can function to yield a desired expression product.

A "host cell" includes an individual cell or cell culture which can be or has been a recipient for vector(s) or for incorporation of nucleic acid molecules and/or proteins. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell
5 due to natural, accidental, or deliberate mutation. A host cell includes cells transfected in vivo with a polynucleotide(s) of this invention.

A "cell line" or "cell culture" denotes eukaryotic cells, derived from higher, multicellular organisms, grown or maintained in vitro. It is understood that the descendants of a cell may not be completely identical (either morphologically, genotypically, or phenotypically) to the parent cell.
10 Cells described as "uncultured" are obtained directly from a living organism, and are generally maintained for a limited amount of time away from the organism (i.e., not long enough or under conditions for the cells to undergo substantial replication).

As used herein, "expression" includes transcription and/or translation.

"Heterologous" means derived from (i.e., obtained from) a genotypically distinct entity
15 from the rest of the entity to which it is being compared. For example, a polynucleotide may be placed by genetic engineering techniques into a plasmid or vector derived from a different source, thus becoming a heterologous polynucleotide. A promoter which is linked to a coding sequence with which it is not naturally linked is a heterologous promoter.

An "isolated" or "purified" polynucleotide, polypeptide or cell is one that is
20 substantially free of the materials with which it is associated in nature. By substantially free is meant at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90%, even more preferably at least 99%, and even more preferably at least 99.9% free of the materials with which it is associated in nature. As used herein, an "isolated"
polynucleotide or polypeptide also refers to recombinant polynucleotides or polypeptides,
25 which, by virtue of origin or manipulation: (1) are not associated with all or a portion of a polynucleotide or polypeptide with which they are associated in nature, (2) are linked to a polynucleotide or polypeptide other than that to which they are linked in nature, or (3) do not occur in nature, or (4) in the case of polypeptides, arise from expression of recombinant polynucleotides. Thus, for example, an isolated substance may be prepared by using a
30 purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per volume of solution, by specific activity or it can be measured in relation to a second, potentially interfering substance present in the source mixture.
Increasing enrichments of the embodiments of this invention are increasingly more preferred.

Thus, for example, a 2-fold enrichment is preferred, 10-fold enrichment is more preferred, 100-fold enrichment is more preferred, 1000-fold enrichment is even more preferred. A substance can also be provided in an isolated state by processes such as chemical synthesis or recombinant expression.

5 A "reagent" polynucleotide, polypeptide, or antibody, is a substance provided for a reaction, the substance having some known and desirable function in the reaction. A reaction mixture may also contain a "target", such as a polynucleotide, antibody, polypeptide, or assembly of polypeptides that the reagent is capable of reacting with. For example, in some types of diagnostic tests, the presence and/or amount of the target in a sample is determined by
10 adding a reagent, allowing the reagent and target to react, and measuring the amount of reaction product (if any).

 "Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogsteen binding, or in any
15 other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of an amplification reaction such as PCR, or the enzymatic cleavage of a polynucleotide by a ribozyme.

20 When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, those polynucleotides are described as "complementary". A double-stranded polynucleotide can be "complementary" to another polynucleotide if hybridization can occur between one of the strands of the first polynucleotide and the second. The degree to which one polynucleotide is complementary with another is quantifiable in terms of the proportion of bases in
25 opposing strands that are expected to form hydrogen bonds with each other, according to generally accepted base-pairing rules of A-T, A-U and G-C.

 A "stable duplex" of polynucleotides, or a "stable complex" formed between any two or more components in a biochemical reaction, refers to a duplex or complex that is sufficiently long-lasting to persist between formation of the duplex or complex and subsequent detection,
30 including any optional washing steps or other manipulation that may take place in the interim.

 A substance is said to be "selective" or "specific" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular cell or substance than it does with alternative cells or substances. An odorant ligand "specifically

binds" to a target if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds to other substances.

As used herein, "naturally occurring," "native," or "wild type" refers to endogenous polynucleotides and the protein(s) expressed thereby. These terms include full-length and processed polynucleotides and polypeptides. Processing can occur in one or more steps, and these terms encompass all stages of processing. For instance, polypeptides having or lacking a signal sequence are encompassed by the invention. "Non-naturally occurring", "non-native", or "non-wild type" refer to all other polynucleotides and polypeptides.

A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made of a target polynucleotide using one or more primers, and a catalyst of polymerization, such as a reverse transcriptase or a DNA polymerase, and particularly a thermally stable polymerase enzyme. Methods for PCR are taught in U.S. Patent Nos. 4,683,195 (Mullis) and 4,683,202 (Mullis et al.). All processes of producing replicate copies of the same polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "amplification."

According to this invention, a "genomic DNA library" is a clone library which contains representative nucleotide sequences from the DNA of a given genome. It is constructed using various techniques that are well known in the art, for instance, by enzymatically or mechanically fragmenting the DNA from an organism, organ, or tissue of interest, linking the fragments to a suitable vector, and introducing the vector into appropriate cells so as to establish the genomic library. A genomic library contains both transcribed DNA fragments as well as nontranscribed DNA fragments.

In comparison, a "cDNA library" is a clone library that differs from a genomic library in that it contains only transcribed DNA sequences and no nontranscribed DNA sequences. It is established using techniques that are well known in the art, i.e., selection of mRNA (e.g. by polyA) making single stranded DNA from a population of cytoplasmic mRNA molecules using the enzyme RNA-dependent DNA polymerase (i.e., reverse transcriptase), converting the single-stranded DNA into double-stranded DNA, cloning the resultant molecules into a vector, and introducing the vector into appropriate cells so as to establish the cDNA library. Alternately, a cDNA library need not be cloned into a vector and/or established in cells, but can be screened using PCR with gene-specific primers, as is well known in the art.

An "individual" is a vertebrate, preferably a mammal, more preferably a human.

General Techniques

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as: "Molecular Cloning: A Laboratory Manual", second edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984); "Animal Cell Culture" (R.I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller & M.P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987 and annual updates); "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994); "Current Protocols in Immunology" (J.E. Coligan et al., eds., 1991).

Basis for identification and description of the polynucleotides and polypeptides

The polynucleotide sequences were identified using oligonucleotide primers which were complementary to OR membrane-spanning regions. A number of different primers were used to elicit a variety of nucleotide sequences which encode polypeptides involved in olfactory sensation. The identification and isolation of nucleotide sequences which encode polypeptides involved in olfactory sensation and the polypeptides that they encode is vital for determining the response of receptors to odorant molecules, the elucidation of scent representations, profiles, or fingerprints, the reproduction of scent representations, profiles, or fingerprints and the editing of scent representations, profiles, or fingerprints.

Polynucleotides encoding polypeptides involved in olfactory sensation

The present invention provides isolated polynucleotides encoding polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. These polynucleotides are isolated and/or produced by chemical and/or recombinant methods, or a combination of these methods. The present invention includes polynucleotides isolated from the human olfactory epithelium which encode polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. Unless specifically stated otherwise,

“polynucleotides” shall include all embodiments of the polynucleotides of this invention.

These polynucleotides are useful as probes, primers, in expression systems, and, in a preferred embodiment, in screening methods as described herein. In one embodiment the polynucleotides of the present invention can be isolated by creating a cDNA library using
5 template RNA from human olfactory epithelium tissue. A detailed example is related in Example 1, below.

The advantage of constructing a cDNA library for isolation of the desired nucleotide sequences is that the likelihood of obtaining pseudogenes is greatly reduced compared to using a genomic DNA library for the same purpose. cDNA libraries contain only mRNA expressed
10 in the tissue used for the construction of the library, in this case, the human olfactory epithelium. The preferred olfactory epithelium tissue should express only those nucleotide sequences which are relevant for olfactory function, thereby excluding nonfunctioning pseudogenes and also GPCRs which may be similar in primary structure (amino acid sequence) but are not encoded in OSNs. As the number of GPCRs utilized in human signal transduction
15 pathways is extremely wide and varied, cDNA libraries constructed using olfactory tissue are preferable for isolating nucleotide sequences that encode polypeptides which are involved in olfactory sensation, inasmuch as genomic libraries can contain abundant nucleotide sequences which encode for a variety of GPCRs performing numerous functions, and are likely to contain pseudogenes.

20 The isolation of polynucleotide sequences which encode polypeptides involved in olfactory sensation is described in Example 1. Accordingly, this invention provides isolated polynucleotides that contain sequences encoding polypeptides or portions thereof which are involved in olfactory sensation, wherein the polypeptide is at least 10 amino acids in length, and wherein the polynucleotide sequences are depicted in SEQ ID NOs:1-73 and SEQ ID
25 NOs:111-152.

The invention includes modifications to said polynucleotides described above such as deletions, substitutions, additions, or changes in the nature of any nucleic acid moieties. A “modification” is any difference in nucleotide sequence as compared to a polynucleotide shown herein to encode a polypeptide involved in olfactory sensation, and/or any difference in
30 the nucleic acid moieties of the polynucleotide(s), wherein such a modified polynucleotide encodes a polypeptide involved in olfactory sensation or a variant of said polypeptide that is useful in the practice of the invention. Such changes can be useful to facilitate cloning and modify expression of polynucleotides encoding polypeptides which are involved in olfactory

sensation. Such changes also can be useful for conferring desirable properties to the polynucleotide(s), such as stability. The definition of polynucleotide provided herein gives examples of these modifications. Hence, the invention also includes variants of the nucleic acid sequences disclosed herein, which include nucleic acid substitutions, additions, and/or deletions.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, including polynucleotides that are full-length, processed, coding, non-coding (including flanking region) or portions thereof, provided that these polynucleotides contain a region encoding at least a portion of a polypeptide involved in olfactory sensation.

(That is, the region encodes a functional fragment of an olfactory receptor or other polypeptide involved in olfactory sensation.) Also embodied are the mRNA, cDNA and genomic DNA sequences and fragments thereof that include a polynucleotide sequence comprising a coding sequence for a portion of a polypeptide involved in olfactory sensation.

Genes encoding human olfactory receptors, and optionally including related genomic sequences such as regulatory sequences, can be obtained using olfactory receptor cDNAs as hybridization probes. Under high stringency hybridization conditions, an OR cDNA will hybridize to its cognate OR gene. Use of lower stringency hybridization conditions allows the isolation of OR genes that are related to, but not identical with, the gene corresponding to a particular OR cDNA.

Conditions for hybridization are well-known to those of skill in the art and can be varied within relatively wide limits. Hybridization stringency refers to the degree to which hybridization conditions disfavor the formation of hybrids containing mismatched nucleotides, thereby promoting the formation of perfectly matched hybrids or hybrids containing fewer mismatches; with higher stringency correlated with a lower tolerance for mismatched hybrids. Factors that affect the stringency of hybridization include, but are not limited to, temperature, pH, ionic strength, and concentration of organic solvents such as formamide and dimethylsulfoxide. As is well known to those of skill in the art, hybridization stringency is increased by higher temperatures and/or lower ionic strengths. See, for example, Ausubel et al., supra; Sambrook et al., supra; M.A. Innis et al. (eds.) PCR Protocols, Academic Press, San Diego, 1990; B.D. Hames et al. (eds.) Nucleic Acid Hybridisation: A Practical Approach, IRL Press, Oxford, 1985; and van Ness et al., (1991) Nucleic Acids Res. 19:5143-5151. The degree of stringency can be adjusted not only during a hybridization reaction, but also in post-hybridization washes, as is known to those of skill in the art.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, functionally equivalent variants and derivatives of full-length polypeptides involved in olfactory sensation and functionally equivalent fragments. For instance, changes in a DNA sequence that do not change the encoded amino acid sequence, as well as those that result in conservative substitutions of amino acid residues, non-deleterious non-conservative substitutions, one or a few amino acid deletions or additions, and substitution of amino acid residues by amino acid analogs, will not significantly affect properties of the encoded polypeptide. Polypeptides homologous to the polypeptides encoded by the polynucleotides described herein can also be identified using algorithms and methods well-known to those of skill in the art, such as those described in Ausubel, "Current Protocols in Molecular Biology," Chapter 19; see also Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649-656. A preferred method of determining homology is the BLAST set of similarity search programs (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410. Polypeptides which are 40% homologous, 50% homologous, 60% homologous, 70% homologous, 80% homologous, 90% homologous, 95% homologous, or 99% homologous to the polypeptides encoded by the polynucleotides described herein are encompassed by the invention.

Nucleotide substitutions that do not alter the amino acid residues encoded can be useful for optimizing gene expression in different systems. Suitable substitutions are known to those of skill in the art and are made, for instance, to reflect preferred codon usage in the particular expression systems. In another example, alternatively spliced polynucleotides can give rise to different functionally equivalent fragments or variants of an polypeptide involved in olfactory sensation. Alternatively processed polynucleotide sequence variants are defined as polynucleotide sequences corresponding to mRNAs that differ in sequence from one another but are derived from the same genomic region, for example, mRNAs that result from: 1) the

use of alternative promoters; 2) the use of alternative polyadenylation sites; and/or 3) the use of alternative splice sites.

Preparation of polynucleotides involved in olfactory sensation

5 The polynucleotides of this invention can be obtained using chemical synthesis, recombinant methods, or PCR.

Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to produce a desired DNA sequence.

10 For preparing polynucleotides which encode polypeptides involved in olfactory sensation using recombinant methods, a polynucleotide comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification. Polynucleotides may be inserted into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct
15 uptake, endocytosis, transfection, F-mating, particle bombardment, liposome mediation, or electroporation. Once introduced, an exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. The polynucleotide encoding a polypeptide involved in olfactory sensation can be isolated from the host cell by methods well known within the art. See, e.g., Sambrook et al. (1989).

20 Alternatively, PCR allows amplification of DNA sequences. PCR technology is well known in the art and is described in U.S. Pat. Nos. 4,683,195, 4,800,159, 4,754,065 and 4,683,202, as well as *PCR: The Polymerase Chain Reaction*, Mullis et al. eds., Birkhausw Press, Boston (1994).

RNA can be obtained in a number of ways in an appropriate vector and the vector is
25 transformed into a suitable host cell. When the inserted DNA is transcribed into RNA, the RNA can then be isolated using methods well known to those of skill in the art, as set forth in Sambrook et al., (1989), for example. RNA can also be obtained through in vitro reactions. For example, the polynucleotide, which encodes a polypeptide involved in olfactory sensation, can be inserted into a vector that contains appropriate transcription promoter sequences.
30 Commercially available RNA polymerases will specifically initiate transcription at their promoter sites and continue the transcription process through the adjoining DNA polynucleotides. Placing the polynucleotide sequences which encode polypeptides involved in

olfactory sensation between two such promoters allows the generation of sense or antisense strands of desired RNA.

5 *Cloning and expression vectors comprising polynucleotide sequences encoding polypeptides involved in olfactory sensation*

 The present invention further includes a variety of vectors containing polynucleotides encoding polypeptides involved in olfactory sensation. These vectors can be used for expression of recombinant polypeptides as well as a source of polynucleotides which encode polypeptides involved in olfactory sensation. Cloning vectors can be used to obtain replicate
10 copies of the polynucleotides, which encode polypeptides involved in olfactory sensation, they contain, or as a means of storing the polynucleotides in a depository for future recovery. Expression vectors (and host cells containing these expression vectors) can be used to obtain polypeptides produced from the polynucleotides they contain. Suitable cloning and expression
15 vectors include any known in the art, e.g., those for use in in vitro, bacterial, mammalian, yeast and insect expression systems. Specific vectors and suitable host cells are known in the art and need not be described in detail herein. For example, see Gacesa and Ramji, *Vectors*, John Wiley & Sons (1994).

 Cloning and expression vectors typically contain a selectable marker (for example, a gene encoding a protein necessary for the survival or growth of a host cell transformed with the
20 vector), although such a marker gene can be carried on another polynucleotide sequence co-introduced into the host cell. Only those host cells into which a selectable marker has been introduced will survive and/or grow under selective conditions. Typical selectable markers encode protein(s) that (a) confer resistance to antibiotics or other toxins substances, e.g., ampicillin, neomycin, methotrexate, etc.; (b) complement auxotrophic deficiencies; or (c)
25 supply critical nutrients not available from complex media. The choice of the proper marker gene will depend on the host cell, and appropriate genes for different hosts are known in the art. Cloning and expression vectors also typically contain a replication system recognized by the host.

 Suitable cloning vectors may be constructed according to standard techniques, or may
30 be selected from a large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self-replicate in an appropriate host, may possess a single target for one or more particular restriction endonucleases, and/or may carry genes for a marker

that can be used in selecting clones containing the vector. Suitable examples include plasmids and bacterial viruses, e.g., pUC18, pUC19, m13mp18, m13mp19, pBR322, pMB9, ColE1, pCR1, RP4, phage DNAs, and shuttle vectors such as pSA3 and pAT28. These and many other cloning vectors are available from commercial vendors such as BioRad, Stratagene, and
5 Invitrogen.

Expression vectors generally are replicatable polynucleotide constructs that contain a polynucleotide encoding an polypeptide involved in olfactory sensation of interest. The polynucleotide, which encodes a polypeptide involved in olfactory sensation, encoding the polypeptide is operatively linked to suitable transcriptional controlling elements, such as
10 promoters, enhancers and terminators. For expression (i.e., translation), one or more translational controlling elements are also usually required, such as ribosome binding sites, translation initiation sites, and stop codons. These controlling elements (transcriptional and translational) may be derived from the gene encoding polypeptides involved in olfactory sensation, or they may be heterologous (i.e., derived from other genes and/or other organisms).
15 A polynucleotide sequence encoding a signal peptide can also be included to allow a polypeptide involved in olfactory sensation to cross and/or lodge in cell membranes or be secreted from the cell. A number of expression vectors suitable for expression in eukaryotic cells including yeast, insect, avian, plant and mammalian cells are known in the art. Common vectors, such as YEpl3 and the Sikorski series pRS303-306, 313-316, 423-426 can also be
20 used. Vectors pDBV52 and pDBV53 are suitable for expression. Another example of an expression vector/host cell system is the baculovirus (e.g., nuclear polyhedrosis virus)/insect cell (e.g., sf9 cells) system.

Human olfactory receptor polypeptides are expressed from olfactory receptor cDNA by
methods well-known to those of skill in the art. A cDNA or portion thereof is inserted in an
25 expression vector using standard molecular cloning techniques. Coupled in vitro transcription and translation of such a vector results in expression of the OR protein encoded by the cDNA. In vivo expression of a OR polypeptide is accomplished by inserting an OR cDNA into a eucaryotic or procaryotic expression vector, of which many are known in the art, to generate an OR expression construct. The OR expression construct is introduced into an appropriate
30 host cell in which the OR sequences are expressed (by transcription and translation) and optionally secreted, and the expressed OR polypeptide is obtained from the cell growth medium and/or from cell lysates.

A number of expression vectors are known in the art. Prokaryotic expression vectors include, but are not limited to, T7 RNA polymerase/T7 promoter-based vectors, bacteriophage λ -based vectors and various types of fusion vectors. Fusion vectors include, but are not limited to, lacZ and trpE fusion vectors, maltose binding protein fusion vectors, glutathione-S-transferase fusion vectors, and thioredoxin fusion vectors. Baculovirus-based vectors are used for expression in insect cell systems. Expression in mammalian cells (such as HEK, COS and CHO cells) utilizes vectors containing a mammalian origin of replication (such as, for example, a SV40 origin), an efficient promoter (optionally including one or more enhancer sequences), mRNA processing signals (e.g., splice sites and polyadenylation sites), one or more selectable markers, and optionally a prokaryotic replicon to allow propagation and manipulation of the construct in prokaryotic cells. Alternatively, expression in mammalian cells is achieved through the use of any of a number of mammalian viral vectors including, but not limited to, retroviruses, lentiviruses, Semliki Forest viruses, vaccinia viruses, adenoviruses and adeno-associated viruses.

Vectors containing the polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including electroporation, direct injection, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent, such as a virus). The choice of means of introducing vectors or polynucleotides encoding polypeptides involved in olfactory sensation will often depend on the host cell, as will be well known to those of skill in the art.

Host cells transformed with polynucleotides encoding polypeptides involved in olfactory sensation

Another embodiment of this invention are host cells transformed with (i.e., comprising) polynucleotides encoding polypeptides involved in olfactory sensation, and/or vectors having polynucleotide(s) sequences encoding polypeptides involved in olfactory sensation, as described above. Both prokaryotic and eukaryotic host cells may be used. Prokaryotic hosts include bacterial cells, for example *E. coli*, *B. subtilis*, and mycobacteria. Among eukaryotic hosts are yeast, insect, avian, plant and mammalian cells. Host systems are known in the art and need not be described in detail herein.

The host cells of this invention can be used, *inter alia*, as repositories of polynucleotides encoding polypeptides involved in olfactory sensation, and/or vehicles for

production of polynucleotides encoding polypeptides involved in olfactory sensation, and/or polypeptides involved in olfactory sensation . They may also be used as vehicles for *in vivo* delivery of polypeptides involved in olfactory sensation .

5 ***Uses for and methods using polynucleotides encoding polypeptides involved in olfactory sensation***

To determine whether a vector containing polynucleotides is capable of expressing in eukaryotic cells, cells such as, for example, COS-7 (primate origin), CHO (rodent origin), HEK-293 (human origin), or HeLa (human origin) cells can be transfected with the vector.

- 10 Expression of a polypeptide(s) encoded by the vector is then determined by, for example, RIA, ELISA, immunofluorescence of fixed cells, or western blotting of cell lysate using an antibody as a probe. Antibodies can be obtained using, as immunogen, peptide sequences synthesized from the protein sequences encoded by the known polynucleotide sequence. Polypeptides can be purified by, for example, phase partitioning, affinity methods, gel filtration and ion
- 15 exchange, as well as additional methods known by those skilled in the art. Further characterization of the expressed polypeptide can be achieved by purification of the polypeptide using techniques known in the art.

Polypeptides involved in olfactory sensation

- 20 The present invention encompasses polypeptides involved in olfactory sensation. Expression of said polypeptides is localized in the olfactory neurons located in the olfactory epithelium, as described earlier. The polypeptides may comprise any novel sequence encoded by a nucleotide sequence as depicted in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152.

- 25 The invention includes modifications to polypeptides involved in olfactory sensation including functionally equivalent fragments of the polypeptides involved in olfactory sensation which do not significantly affect their properties and variants which may have enhanced or decreased activity. Collectively, these modifications may be termed "analogs" of or a fragment of polypeptides involved in olfactory sensation. Modification of polypeptides is routine practice in
- 30 the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or use of chemical analogs. Amino acid residues which can be conservatively substituted for

one another include but are not limited to: glycine/alanine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; serine/threonine; lysine/arginine; and phenylalanine/tyrosine. Such conservative substitutions are known in the art, and preferably, the amino acid substitutions would be such that the substituted amino acid would possess similar chemical properties as that of the original amino acid. These polypeptides also include glycosylated and non-glycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with different sugars, acetylation, and phosphorylation. Amino acid modifications can range from changing or modifying one or more amino acids to complete redesign of a region. Other methods of modification include using coupling techniques known in the art, including, but not limited to, enzymatic means, oxidative substitution and chelation. Modified polypeptides involved in olfactory sensation are made using established procedures in the art.

The invention also encompasses fusion proteins comprising one or more polypeptides involved in olfactory sensation. For purposes of this invention, a fusion protein contains one or more polypeptides involved in olfactory sensation and another amino acid sequence to which it is not attached in the native molecule, for example, a heterologous sequence or a homologous sequence from another region. Useful heterologous sequences include, but are not limited to, sequences that provide for secretion from a host cell, intracellular trafficking, and stability/degradation. Other useful heterologous sequences are ones which facilitate purification. Examples of such sequences are known in the art and include those encoding epitopes such as Myc, HA (derived from influenza virus hemagglutinin), His-6, or FLAG. Other heterologous sequences that facilitate purification are derived from proteins such as glutathione S-transferase (GST), maltose-binding protein (MBP), or the Fc portion of immunoglobulin.

Preparation of polypeptides involved in olfactory sensation

The polypeptides of this invention can be made by procedures known in the art. The polypeptides can be produced by recombinant methods (i.e., single or fusion polypeptides) or by chemical synthesis. Polypeptides, especially shorter polypeptides up to about 50 amino acids, are conveniently made by chemical synthesis. Methods of chemical synthesis are known in the art and are commercially available. For example, a polypeptide can be produced by an automated polypeptide synthesizer employing the solid phase method. Polypeptides can also be made by chemical synthesis using techniques known in the art.

Polypeptides can also be made by expression systems, using recombinant methods.

The availability of polynucleotides encoding polypeptides permits the construction of expression vectors encoding intact (i.e., native) polypeptide, functional equivalents and functional fragments thereof, modified forms or recombinant forms. A polynucleotide
5 encoding the desired polypeptide, or a fusion protein, can be ligated into an expression vector suitable for any convenient host. Both eukaryotic and prokaryotic host systems can be used. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification or isolation of the polypeptides expressed in
10 host systems can be accomplished by any method known in the art (e.g. partitioning exclusion, ion exchange chromatograph, gel filtration, etc.). Other controlling transcription or translation segments, such as signal sequences that direct the polypeptide to a specific cell compartment (i.e., for secretion), can also be used. Examples of prokaryotic host cells are known in the art and include, for example, *E. coli* and *B. subtilis*. Examples of eukaryotic host cells are known in the art and include yeast, avian, insect, plant, and animal cells such as COS7, HeLa, CHO,
15 HEK-293 and other mammalian cells.

Alternatively, in vitro expression systems may also be used to produce polypeptides involved in olfactory sensation. A plasmid containing a polynucleotide encoding polypeptides involved in olfactory sensation, under the control of an appropriate promoter, can be transcribed and the resultant RNA translated in vitro through the use of commercially
20 available reagents. Such methods can be used to produce relatively pure samples of the polypeptide and are known in the art.

Preferably, the polypeptides are at least partially purified from other cellular constituents. In one embodiment, the polypeptides are at least 70%, more preferably at least 80%, even more preferably at least 90% or most preferably at least 95% pure. In this context,
25 purity can be calculated as a weight percent of the total protein content of the preparation. More highly purified polypeptides may also be obtained and are encompassed by the present invention. Methods of protein purification are known in the art and are not described in detail herein. For membrane-bound proteins, the lipid content of the preparation, which is required to maintain the structure and function of the protein, is excluded from the purity calculation. That
30 is, if a preparation weighing 10 mg has 5 mg lipid, 4 mg of desired protein, and 1 mg of undesired proteins, the purity is calculated as 80% (desired protein content divided by total protein content). Preparations of biological or synthetic molecules suitable for maintaining structure and function of membrane proteins are described in Etemadi AH (1985) *Adv Lipid*

Res 1985;21:281-428; Villalobo A (1990) *Biochimica Et Biophysica Acta*, 1017(1):1-48; Montal M (1987) *Journal Of Membrane Biology* 98(2): 101-115; Scotto AW et al. (1987) *Biochemistry* 26(3): 833-839; Jain MK and Zakim D (1987) *Biochimica Et Biophysica Acta* 906(1): 33-68; Czerski L and Sanders CR (2000) *Anal Biochem* 284(2):327-33 (lipid-detergent mixtures or "bicelles"); Hrafnisdottir S and Menon AK (2000) *J Bacteriol* 182(15):4198-206 (proteoliposomes); Puu G et al. (2000) *Biosens Bioelectron* 15(1-2):31-41 (protein-lipid preparations on solid surfaces); Schafmeister CE et al. (1993) *Science* 262(5134):734-8 ("peptitergents").

10 *Uses of polypeptides involved in olfactory sensation*

The polypeptides of this invention have a variety of uses. They can be used, for example, to screen odorant ligands in order to determine the scent representations, scent profiles or scent fingerprints of particular odorant molecules and further to characterize the effect of functional groups and chemical characteristics on perceived smell. Methods for screening odorant compounds using odorant receptors in neuronal cells are known in the art (Firestein et al., WO 98/50081; Duchamp-Viret *et al.*, *Science* 1999, 284 2171-2174; Sato *et al.*, *J. Neurophys.* 1994 72 2980-2989; Malnic *et al.*, *Cell* 1999 96 713-723; Zhao *et al.*, *Science* 1998 279, 237-242). There are also methods which can be employed to screen odorant compounds which do not require neuronal cells and are known in the art (Kauvar et al., U. S. Pat. No. 5,798,275; Kiefer *et al.*, *Biochemistry* 1996 35 16077-16084; Krautwurst *et al.*, *Cell* 1998 95 917-926),

Analysis of the scent can be performed in a number of ways. Various embodiments of the scent analysis system are presented. Examples of how these embodiments might operate are also presented, although it should be emphasized that the invention is not limited by any particular theory of olfactory perception or scent analysis.

Olfactory Space

The sensory subsystem comprises a series of olfactory receptors, which selectively bind with the chemical component(s) making up the scent. The scent can be characterized in terms of which of the approximately 1,000 olfactory receptors the scent component(s) bind to, and the strength of the interaction of the component(s) with those receptors. Each olfactory receptor can be considered an orthogonal basis vector; the entire set of olfactory receptors can be considered a set of basis vectors spanning "olfactory space." This is analogous to vectors

pointing along the x, y, and z directions in three-dimensional space, where any point in space can be represented by a combination of the x, y, and z basis vectors (with each of the x, y, and z vectors multiplied by the appropriate scalar quantity). The intensity of interaction of a scent with an olfactory receptor determines the magnitude of the vector along that particular "axis" in olfactory space. Thus, every scent can be uniquely described by a vector representation in olfactory space.

A representation of a scent in such a manner that the scent can later be re-created is defined as scent profiling. The aforementioned vector representation is one example of a scent profile.

Primary Scents

For the purposes of this invention, a receptor primary scent component is defined as a chemical that interacts with one and only one scent receptor. A receptor complex scent component is defined as a chemical that interacts with more than one scent receptor; the receptor complex scent component can interact with each of the scent receptors to different degrees, to equal degrees, or can interact with some receptors to the same degree and others to different degrees.

Olfactory receptors are proteins which fall in the class of seven transmembrane domain G protein-coupled receptors, and are found in olfactory neurons *in vivo*. Binding of an odorant to an olfactory receptor causes second messenger systems to become activated or inhibited in the cell, leading to increased cellular production of second messenger molecules such as cyclic AMP. These second messenger systems in turn lead to the depolarization of the olfactory neuron, or other changes in the state of the neuron, which provides the signal to the nervous system that the odorant has been detected.

With a complete set of receptor primary scent components, any scent can be re-created with the knowledge to the degree to which it interacts with each olfactory receptor. The instant invention encompasses such complete sets of receptor primary scent components. Other embodiments of the invention encompass sets of receptor primary scent component chemicals which provide the ability to re-create a particularly desired subset of scents, but not necessarily all possible scents. Still more embodiments encompass sets of receptor primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

In some cases, a receptor complex scent will be an acceptable approximation to a receptor primary scent. That is, if a given receptor complex scent interacts with a first scent receptor strongly, but interacts with other scent receptors less strongly, it can be considered an approximation to a receptor primary scent component for the first receptor. Such a receptor complex scent component is described by the term receptor quasi-primary scent component. One embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating all scents. Another embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating a particularly desired subset of scents, but not necessarily all possible scents. Yet another embodiment encompasses sets of receptor quasi-primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

The identification of receptor primary or quasi-primary scent component chemicals provides the most conceptually straightforward method of re-creating scents. However, another embodiment of the invention encompasses the use of receptor complex scent components for re-creating scents. An example of such an embodiment would be re-creation of a scent that activates olfactory receptors designated OR1, OR2, OR3, OR4, OR5 and OR6 (for the sake of illustration, it is assumed that the olfactory receptors are stimulated to an equal extent). If one is in possession of two receptor complex scent component chemicals (RCSC's) where RCSC1 activates OR1 and OR5, and RCSC2 activates OR2, OR3, OR4, and OR6, then one can reproduce the original scent by mixing RCSC1 and RCSC2 to re-create the original olfactory receptor activation profile. In practice, the profiles of various receptor complex scent components will be much more complicated than the forgoing example, and components which inhibit olfactory activation as well as stimulate activation can be included in the sets. However, once receptor activation profiles of sufficient receptor complex scent components are known, computer algorithms can be utilized to create the appropriate combination of receptor complex scent components. Using vector representations of the olfactory receptor activation profiles for a set of receptor complex scent components, one can create linear combinations of such receptor complex scent components in order to represent a particular scent. For the example given above, such a vector representation would look like (1, 0, 0, 0, 1, 0) for the first receptor complex scent component and (0, 1, 1, 1, 0, 1) for the second receptor

complex scent component, while the vector representation of the scent to be re-created is (1, 1, 1, 1, 1, 1). If x_1 and x_2 are the relative proportions of the first receptor complex scent component and the second receptor complex scent component, respectively, to be combined to re-create the scent, then the problem can be represented as a series of linear equations:

$$\begin{array}{rclcl} 1x_1 & + & 0x_2 & = & 1 \\ 0x_1 & + & 1x_2 & = & 1 \\ 0x_1 & + & 1x_2 & = & 1 \\ 0x_1 & + & 1x_2 & = & 1 \\ 1x_1 & + & 0x_2 & = & 1 \\ 0x_1 & + & 1x_2 & = & 1 \end{array}$$

and the solutions for x_1 and x_2 are $x_1 = 1$, $x_2 = 1$. Solutions to systems of linear equations have been thoroughly studied and many algorithms are available for implementation on computers, including algorithms which evaluate the accuracy of an approximate solution when an exact solution cannot be determined. (See, e.g., Dettman, J.W., *Introduction to Linear Algebra and Differential Equations*, Dover Pubs., 1986; Press W.H. et al., *Numerical Recipes in C: The Art of Scientific Computing*, 2nd ed., Cambridge University Press, 1993; Vetterling (ed.) *Numerical Recipes in C: The Art of Scientific Computing/Disk V 2.02*, Cambridge University Press, 1997.) These methods can also be used to determine whether a set of receptor complex scent components is suitable for re-creating a given scent. For example, if the scent to be recreated is represented by the vector (1, 1, 1, 1, 1, 2), there will be no solution to the resulting system of linear equations using the two receptor complex scent components in the illustration above. In this instance, one or more additional receptor scent components will need to be identified in order to be able to re-create the scent in terms of the receptor primary scent components. Alternatively, the scent represented by (1, 1, 1, 1, 1, 1) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2). Integers are used in this example for clarity, but the vectors can contain any real number representing a measured intensity; for example, (1.1, 0.997, 1.08, 1.2, 0.88888..., 2.00001) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2).

It will be readily appreciated that the choice of a complete set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating all scents) versus a partial set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating, exactly or approximately, a subset of scents) depends on the application for which scent re-creation is desired.

A special category of receptor scent components are chemicals which bind to a receptor without activating it. If these non-activating chemicals prevent chemicals which do activate the receptors from binding, the non-activating chemicals act to "turn off" those receptors. These non-activating chemicals, or receptor binding antagonists, are particularly useful in editing scents, as they can be added to a scent to attenuate or eliminate particular aspects of the scent. In the vector example above, if a particular receptor antagonist blocks OR2, OR3, and OR4, but not OR1, OR5 or OR6, then it can be represented in vector format as (0, -1, -1, -1, 0, 0). In the reproduction of (1, 1, 1, 1, 1, 2) from the vectors (1, 0, 0, 0, 1, 0) and (0, 1, 1, 1, 0, 1), the following combination can be used:

$1 \times (1, 0, 0, 0, 1, 0) + 2 \times (0, 1, 1, 1, 0, 1) + 1 \times (0, -1, -1, -1, 0, 0)$ to yield the vector (1, 1, 1, 1, 1, 2). In some instances, enough of a particular receptor binding antagonist is used to eliminate any possibility of activation by a receptor scent component, in which case the vector entry for the receptor(s) which are blocked by that antagonist contains 0 in the vector position corresponding to that receptor(s).

Perceptive primary scents are defined as scents that give a single scent perception, for example, the scent "lemon" as perceived by a human. A perceptive primary scent can be composed of one or more receptor primary scent components, one or more receptor complex scent components, or a mixture of one or more receptor primary scent components and one or more receptor complex scent components. Since perceptive primary scents are to some extent subjective, identification of perceptive primary scents can be performed by using a panel of subjects who evaluate and describe scents. A perceptive complex scent is made up of more than one perceptive primary scent. The boundaries between a perceptive primary scent and a perceptive complex scent are also to some extent subjective; for example, one person may describe a scent as "pizza," while another person may describe the same scent as "sausage, cheese and tomato sauce." That is, one person may perceive a scent as a perceptive primary scent for "pizza," while another person may perceive the same scent as a perceptive complex scent made up of several individual perceptive primary scents. In order to standardize perceptive scents, a panel of five or more, preferably ten or more, more preferably fifty or

more, still more preferably one hundred or more, people can be surveyed to label various perceptive scents. When a plurality, preferably a majority, more preferably 66 2/3 % or greater, still more preferably 95 % or greater, even more preferably 99% or greater, of the panel identifies a scent as the same scent (e.g., of a panel of 100 people, 95 describe a scent as
5 "pizza," while the other 5 describe the scent otherwise), the scent can be labeled as a perceptive scent (the perceptive scent can be primary or complex, depending on whether the panel identifies it as a single scent or a mixture of scents).

In fields where existing classification schemes already exist, the perceptive primary and complex scents can be indexed according to those schemes. For example, the SFP (Société
10 Française des Parfumeurs) has drawn up a classification system based on 5 main groups, subdivided into classes. Such a classification can be used for selecting perceptive primary scents and used as guides for combining the scents.

Selecting Chemicals for Scent Re-creation

15 A scent which has been represented as a set of basis vectors in olfactory space can in principle be re-created simply by mixing the receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components needed to interact the olfactory receptors in the same pattern as the original scent. Such an approach requires 1) a method to generate a representation of the original scent in olfactory space, and 2) suitable
20 receptor primary scent component chemicals which can be mixed in the appropriate manner.

Identification of receptor scent components can be performed by various methods. One such method assays the interaction of candidate components with each olfactory receptor. The receptors can be expressed *in vitro* and assays can be set up to monitor the interaction of
various candidate components with each individual receptor. Chemicals which interact with
25 one and only one olfactory receptor are receptor primary scent components, while chemicals which interact with more than one olfactory receptor are receptor complex scent components (and can possibly be receptor quasi-primary scent components, depending on the interaction profile it displays with the olfactory receptors). Such an approach can use methods known in the art, for example those of Breer *et al.*, Ann. N. Y. Acad. Sci. (1998) 855:175-81 or Malnic *et al.*, Cell (1999) 96(5):713-23. Breer *et al.* expressed olfactory receptors in Sf9 cells and
30 evaluated the second-messenger response to various odorants. Malnic *et al.* isolated olfactory neurons from mice and utilized calcium imaging to study the response of the neurons to different odorants, while using RT-PCR to determine which olfactory receptor was expressed

in the neuron under study. U.S. Patent No. 5,798,275 describes a method for evaluating interaction of compounds with members of a reference panel of proteins. WO 98/50081 discloses methods for detecting particular odorant ligand specificity for particular odorant receptors in nasal epithelium tissue of mammals such as rats and mice.

5

Selection of Receptor Primary Scents by *in silico* Methods

An alternative method utilizes *in silico* screening techniques--that is, computer simulation methods--for selecting candidate components. Protein-ligand screening can be used to select compounds which bind to particular receptors in order to identify receptor primary
10 scent components. Examples of such programs are DOCK, AutoDock, GOLD, FlexX, LUDI, GROWMOL, and HOOK. (See Wang, J., Kollman, P.A., Kuntz I.D., "Flexible ligand docking: a multistep strategy approach," *Proteins* 36(1):1-19 (1999) and references therein.) These programs function by taking a protein structure and either matching compounds of known structure to the protein structure to determine the protein-ligand interaction, or by
15 "growing" a molecule in the active site or binding site of a protein to determine what molecule will best interact with the protein.

Olfactory receptor proteins are membrane proteins, and experimental determination of the three-dimensional structures of membrane proteins has lagged the corresponding structural determination of water-soluble proteins for various reasons. However, alternative methods for
20 constructing the three-dimensional structures of proteins are available. The primary (amino acid) sequences of many olfactory receptors are known. This information can be used to model a three-dimensional structure of a receptor protein using various algorithms and computer programs known in the art. The resulting model structure can then be used as the basis for
evaluating interaction of candidate components with the receptor.

25 Alternatively, given known chemical structures which give rise to a particular odor, analysis of the structures can indicate the particular portion of the chemical structure which is responsible for the odor. This is analogous to "pharmacore analysis" used in medicinal chemistry to determine the important portion of drugs.

Methods for developing compounds which bind to receptors and other proteins of
30 known structure, and determining interactions between ligands and receptors, are described in various references. The DOCK program evaluates the fit of a ligand into a protein molecule of known structure (see Gschwend, D.A., Good, A.C. and Kuntz, I.D., "Molecular Docking Towards Drug Discovery", *J. Mol. Recognition* 9, 175-86 (1996); Kuntz, I.D., Meng, E.C., and

B.K. Shoichet, "Structure-Based Strategies For Drug Design and Discovery", *Acc. Chem. Res.* 27, 117-123 (1994); and Kuntz, I.D., "Structure-based strategies for drug design and discovery", *Science* 257, 1078-1082 (1992); see also

<http://www.cmpharm.ucsf.edu/kuntz/dock.html>). Using a known (or modeled) structure of an

5 olfactory receptor, DOCK can be used to screen for compounds which bind to the receptor.

The program AMBER (see Cornell, WD, Cieplak P, Bayly CI, Gould IR, Merz KM Jr, Ferguson DM, Spellmeyer DC, Fox T, Caldwell JW and Kollman PA. "A second generation force field for the simulation of proteins and nucleic acids," *Journal of the American Chemical Society* 117, 5179-5197 (1995); Computer Simulation of Biomolecular Systems, A. Wilkinson,

10 P. Weiner, W. Van Gunsteren, eds. Volume 3, p. 83-96, P. Kollman, R. Dixon, W. Cornell, T. Fox, C. Chipot and A. Pohorille; Bayly CI, Cieplak P, Cornell WD and Kollman PA. "A well-behaved electrostatic potential based method using charge restraints for deriving atomic charges - the RESP model," *Journal of Physical Chemistry* 97(40), 10269-10280 (1993);

Cornell WD, Cieplak P, Bayly CI and Kollman PA. "Application of RESP charges to calculate conformational energies, hydrogen bond energies, and free energies of solvation," *Journal of the American Chemical Society* 115(21), 9620-9631 (1993); see also

<http://www.amber.ucsf.edu/amber/amber.html>) can be used to calculate more precise

interaction energies between candidate ligands. Other examples of such methods are described in, for example, U.S. Patent No. 5,866,343, directed to determining the energetically favorable

20 binding site between two molecules; U.S. Patent No. 5,854,992, a system and method for structure-based drug design which takes into account binding free energy as it "grows" candidate molecules into a receptor binding site; and U.S. Patent No. 5,495,423, which describes a method for ligand design (principally applicable to peptidic ligands).

The foregoing methods typically depend on a known three-dimensional structure for the
25 receptor. When such a structure cannot or has not been determined experimentally, a structure can be modeled using computer algorithms. Blundell TL, Sibanda BL, Sternberg MJ, Thornton JM, "Knowledge-based prediction of protein structures and the design of novel molecules," *Nature* 326(6111):347-52 (1987); Shortle D, "Structure prediction: The state of the art," *Curr Biol* 9(6):R205-9 (1999), Morea V, Leplae R, Tramontano A, "Protein structure prediction and design," *Biotechnol Annu Rev* 4:177-214 (1998) and Onuchic JN, Luthey-Schulten Z, Wolynes PG, "Theory of protein folding: the energy landscape perspective," *Annu Rev Phys Chem* 30 48:545-600 (1997) address various methods of predicting protein structure from sequence data.

Various implementations for predicting protein structure from amino acid sequences are discussed in U.S. Patent Nos. 5,878,373 and 5,884,230.

If the structure, or even the identity, of the targeted receptor cannot be determined, alternative computational techniques can be used to generate information regarding possible
5 ligands which will interact with the receptor. Quantitative structure-activity relationships (QSAR; see Green, S.M. and Marshall, G.R., "3-D QSAR: A current perspective," Trends Pharmacol Sci 16:285 (1995); and 3D QSAR in Drug Design: Theory, Methods and Applications, Kubinyi, H. Ed.; Escom, Leiden.), including QSAR refinements such as comparative molecular field analysis (ComFA) (Cramer, R. D. et al. "Comparative Molecular
10 Field Analysis ComFA 1. Effect Of Shape On Binding Of Steroids To Carrier Proteins," *J. Am. Chem. Soc.* 110: 5959 (1988)); and pharmacophore mapping (Martin YC, Bures MG, Danaher EA, DeLazzer J, Lico I, Pavlik PA, "A fast new approach to pharmacophore mapping and its application to dopaminergic and benzodiazepine agonists," *J Comput Aided Mol Des* 7(1):83-102 (1993)) have been used to design pharmacophores that can interact with the receptor. U.S.
15 Patent No. 5,699,268 provides a method for producing computer-simulated receptors which functionally mimic biological receptors; the simulated receptors are essentially abstractions of structurally useful information from compounds which are known to interact with a receptor. U.S. Patent No. 5,901,069 describes a method of automatically refining a set of chemicals using structure/activity data. U.S. Patent No. 5,862,514 describes a method of simulating
20 synthesis of compounds of desired biological activity and evaluating their activity via further simulations.

Application of structure-function relationships to classification of odors has been described by Chastrette M., Rallet E. "Structure-minty odour relationships: Suggestion of an
interaction pattern," *Flavour and Fragrance Journal*, 13(1):5-18 (1998); Chastrette M., De
25 Saint Laumer J.Y., Peyraud J.F., "Adapting the structure of a neural network to extract chemical information. Application to structure-odour relationships," *SAR QSAR Environ Res* 1 (2-3):221-231 (1993), Chastrette M., "Trends in structure-odor relationships," *SAR QSAR Environ Res* 6(3-4):215-254 (1997) and Jain et al., "A shape-based machine learning tool for drug design," *J Comput Aided Mol Des* 8(6):635-652 (1994). These methods can be useful in
30 determining the "chemical distance" between odors. For example, isoamyl acetate is typically experienced as a banana-like odor, while octyl acetate is typically experienced as an orange-like odor, which gives a measure of how the chain length of the alkoxy portion of the ester influences perception.

Olfactory Receptors and Libraries of Olfactory Receptors

The olfactory receptors of the invention can be used to analyze and describe the interaction of scent odorant molecules with each receptor. This can be done individually, receptor-by-receptor and odorant molecule by odorant molecule. However, a combinatorial approach provides a much more powerful method of analyzing and describing the interaction of scent odorant molecules with olfactory receptors.

In one embodiment, the invention comprises libraries of olfactory receptors. These libraries are used to screen compositions for interaction with receptors. A composition can be a single compound (essentially a pure chemical), or a mixture of two or more compounds or chemicals. The compositions can be presented to the library in vapor form, or in solutions, typically aqueous solutions.

The method for determining the binding pattern of a composition with olfactory receptors comprises the steps of: exposing the composition to an olfactory receptor library; and determining whether the composition binds to each olfactory receptor of the library, thereby determining the overall binding pattern of the composition. While it is desirable to determine whether the composition binds to each of the olfactory receptors, in certain cases, determining the binding pattern to a subset of the receptors is suitable. Such a situation can arise if the complete pattern is not needed, or if the experiment cannot determine binding to a receptor for a particular reason. (Determining the binding to a subset is equivalent to reducing the olfactory receptor library to that subset of receptors.)

Typically, the libraries are prepared as arrays, where the position of each olfactory receptor is known on the array. The arrays can take the form of multiwell plates, solid substrates such as chips or wafers, or any other form allowing identification of the receptor location. The arrays can be prepared in order to simply assess binding, or can be prepared in order to assess degree of activation as described above, using, for example, the technique of Malnic *et al.*, *Cell* 1999 96, 713-723. Alternatively, an *in silico* array of structures can be prepared, using the known primary structure of the receptors and the modeling techniques described above.

The libraries contain at least two olfactory receptors. In increasing order of preference, the libraries contain at least 5, 10, 20, 30, 40, 50, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1500, 1600, 1800, or 2000 olfactory receptors. The

receptors are presented as ordered arrays. For example, a 96-well plate can contain 96 receptor preparations. Upon exposure to a composition, the plate can be scanned, and the response of each receptor in each well can be evaluated. This leads to a 96-element vector description of the composition in terms of those 96 olfactory receptors.

5 In one embodiment, binding to the olfactory receptors is assessed. In another embodiment, the approximate binding constant of the composition to the olfactory receptors is determined. In yet another embodiment, the degree of activation of the olfactory receptor by the composition is determined. For receptor antagonists, binding will occur, but no activation will occur; the invention embraces the identification of such
10 antagonists.

 The compositions for use are varied. A set of all volatile compounds can be used. A standard set of perfumes or odorants can be used. A set of commercially used scents can be used. Sets of compounds particularly useful in the invention are disclosed in co-pending United States Patent Application Serial No. 09/620,753. However, it must be emphasized
15 that the invention is not limited to any one set or classification of compounds.

 Preferred subsets of olfactory receptor polynucleotide sequences include:

 SEQ ID NOS: 163, 331, 414, 425, 672, 762, 919, and 1027;

 SEQ ID NOS: 809 and 1067;

 SEQ ID NO: 744;

20 SEQ ID NOS: 207, 336, 441, and 615;

 SEQ ID NOS: 157, 168, 197, 221, 250, 334, 340, 412, 413, 459, 491, 618, 690,
694, 759, 760, 761, 767, 819, 860, 872, 873, 917, 936, 939, 940, 947, 952, 958, 959, 1023,
1034, 1038, 1043, and 1044;

 SEQ ID NOS: 783, 785, 882, 888, 922, and 925;

25 SEQ ID NOS: 707, 748, 752, 755, 756, 790, and 997;

 SEQ ID NOS: 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075,
1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, and 1084;

 SEQ ID NOS: 163, 239, 331, 335, 368, 381, 385, 414, 425, 514, 572, 596, 603,
628, 638, 642, 672, 674, 689, 744, 762, 809, 835, 885, 896, 919, 920, 938, 948, 972, 999,
30 1007, 1014, and 1027;

 SEQ ID NOS: 164, 173, 176, 180, 182, 184, 185, 188, 190, 194, 207, 210, 213, 214,
215, 217, 219, 220, 223, 226, 227, 229, 230, 234, 235, 240, 249, 255, 265, 270, 273, 274,

276, 277, 279, 281, 289, 291, 293, 294, 298, 302, 307, 311, 318, 319, 321, 330, 336, 339,
341, 342, 343, 348, 351, 356, 359, 361, 365, 366, 367, 368, 370, 372, 373, 374, 375, 376,
378, 379, 380, 382, 383, 384, 385, 388, 391, 392, 393, 398, 400, 401, 403, 408, 420, 423,
427, 428, 431, 434, 435, 438, 439, 440, 441, 447, 448, 450, 455, 458, 464, 465, 468, 471,
5 473, 474, 475, 478, 479, 481, 482, 484, 485, 492, 494, 499, 502, 508, 511, 512, 513, 515,
526, 532, 534, 541, 543, 545, 546, 550, 552, 553, 557, 558, 560, 563, 564, 568, 572, 576,
582, 583, 584, 585, 586, 588, 599, 600, 605, 606, 607, 608, 609, 610, 615, 620, 621, 631,
632, 636, 638, 640, 642, 645, 648, 650, 651, 652, 654, 656, 657, 661, 662, 664, 668, 679,
680, 686, 687, 689, 691, 696, 699, 700, 702, 706, 713, 720, 721, 723, 729, 734, 738, 745,
10 768, 772, 773, 775, 791, 798, 799, 823, 857, 898, 900, 901, 903, 914, 931, 933, 937, 941,
945, 948, 956, 965, 969, 983, 992, 993, 994, 999, 1003, 1005, 1009, 1010, 1011, 1019,
1028, 1035, 1037, 1052, 1061, 1062, and 1063

SEQ ID NOS: 157, 161, 163, 168, 197, 200, 205, 218, 221, 242, 250, 331, 334,
340, 412, 413, 414, 419, 425, 452, 453, 454, 456, 459, 462, 491, 591, 618, 622, 663, 665,
15 667, 670, 672, 690, 694, 695, 709, 759, 760, 761, 762, 767, 819, 820, 822, 826, 832, 846,
847, 860, 872, 873, 877, 881, 887, 908, 911, 913, 917, 919, 921, 936, 939, 940, 942, 944,
947, 951, 952, 955, 958, 959, 960, 964, 975, 977, 979, 986, 1023, 1027, 1034, 1038, 1043,
1044, 1049, and 1051;

SEQ ID NOS: 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 164, 165, 166,
20 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184,
185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220,
221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238,
240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257,
25 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275,
276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293,
294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311,
312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329,
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650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667,
15 668, 669, 670, 671, 673, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687,
688, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706,
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725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742,
743, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761,
20 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780,
781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798,
799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 810, 811, 812, 813, 814, 815, 816, 817,
818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 836,
837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854,
25 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872,
873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 886, 887, 888, 889, 890, 891,
892, 893, 894, 895, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910,
911, 912, 913, 914, 915, 916, 917, 918, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930,
931, 932, 933, 934, 935, 936, 937, 939, 940, 941, 942, 943, 944, 945, 946, 947, 949, 950,
30 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968,
969, 970, 971, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987,
988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 1000, 1001, 1002, 1003, 1004, 1005,

1006, 1008, 1009, 1010, 1011, 1012, 1013, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, and 1064;

5 and any and all combinations of the foregoing sets.

The polypeptide translation products of those polynucleotide sequences form sets of preferred olfactory receptor polypeptides, as well as any and all combinations of those polypeptide sets. The preferred sets of polypeptide translation products, and any and all combinations thereof, are also preferred sets for use as libraries of olfactory receptors for
10 scent analysis.

Scent Fingerprinting

It will be appreciated that in many instances, analysis of a scent (whether in terms of
15 receptor primary scent components, receptor quasi-primary scent components, receptor complex scent components, or other scent representations) is of great utility in and of itself, in addition to the utility of that analysis in scent re-creation. Thus, another embodiment of the invention encompasses "scent fingerprinting," which comprises analysis of a scent profile when re-creation of that scent may not be necessary or desirable. The distinction between scent
20 profiling, as defined above, and scent fingerprinting, as defined here, is that scent profiling is a representation of a scent relative to a mammalian olfactory system in such a manner as to provide useful information about the interaction of the scent with that olfactory system, such as sufficient information to enable re-creation of the scent from receptor primary scent
25 components. In contrast, scent fingerprinting can, but does not necessarily, provide such information.

Various applications and examples of scent fingerprinting can include, but are not limited to, the following illustrative situations. Natural gas is widely used as a heating and fuel supply, but is in itself odorless. Utility companies routinely add small amounts of odorants such as mercaptans to allow detection of natural gas leaks in households. Should a leak occur
30 at an unattended site, however, potentially dangerous quantities of natural gas can accumulate. In such areas, a device which can recognize odorants would be useful.

Another use of scent fingerprinting is quality control of a manufacturing process. Many food items, such as freshly-baked bread and pastries, sauces, and cheeses, have distinct

odors. A manufacturer can record a scent fingerprint for a given food item, e.g. spaghetti sauce for packaging in jars. The quality of the product can then be monitored at various stages in manufacture and storage, and deviations from the established scent fingerprint can be used to alert the manufacturer to problems in manufacture or storage. Quality control scent fingerprints are not limited to food items, but can be used in any circumstance where a volatile component of an item of manufacture can be used as a quality control indicator, e.g., perfume, deodorants, solvent mixtures, etc.

While scent fingerprints need not be meaningful in terms of a mammalian olfactory system, it will be readily appreciated that a scent profile, which does represent a scent in a manner relevant to an olfactory system, is a special type of scent fingerprint. Additionally, the response of a device which yields a scent fingerprint of an odor (such as the "artificial nose" described in U.S. Pat. Nos. 5,571,401, 5,698,089, 5,788,833, 5,891,398 and 5,911,872) can be calibrated against the response of a mammalian olfactory system in order to transform the scent fingerprint generated by the device into a true scent profile which can be utilized to re-create an odor using receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components. The invention encompasses such data transformations.

Scent Editing

Representation of a scent as a scent profile provides the capability of editing the scent. A scent profile which represents a scent in terms of perceptive primary scent components is the most straightforward representation to edit. An example is the perceptive complex primary scent of "burned pizza" comprised of perceptive primary scent components of sausage, cheese, tomato sauce, and burned dough. In order to edit the scent to provide a more pleasant re-

creation, the perceptive primary scent component of burned dough would simply be eliminated. Other scent profiles can be edited using a knowledge of the perception of a particular components. Using our six-receptor example, suppose that the (1, 0, 0, 0, 1, 0) receptor complex scent component is known to provide an unpleasant aspect of the scent, while the (0, 1, 1, 1, 0, 1) component is known to provide the pleasant aspect of the scent. The first complex scent component can be omitted from the edited scent profile, leaving (0, 1, 1, 1, 0, 1) as the edited scent profile. (This would also alter the index values for scent re-creation, from 1 and 1, to 0 and 1.) More complex editing situations can be manipulated using computer algorithms as discussed above.

Individual scent components can be omitted, added, weakened, or intensified, and different scent components can be adjusted in different manners or degrees, depending on the desired result. The editing can be done interactively, with each edited scent emitted by the emitter module for evaluation by the user, or can be done automatically, with
 5 removal/weakening or addition/intensifying of particular components specified in advance, on either an absolute scale or relative to other components.

The following examples are presented to illustrate, but not to limit, the invention.

EXAMPLES

10 **Example 1: Isolation of human olfactory receptor cDNAs**

Total RNA was extracted from human olfactory epithelium and polyA⁺ RNA was obtained by oligo-dT selection. This RNA served as template for cDNA synthesis using reagents from the SMART cDNA Library construction kit (Clontech K1051-1; Palo Alto, CA). The Superscript IITM reverse transcriptase (Life Technologies, Gaithersburg, MD)
 15 was used for first-strand synthesis.

Double-stranded cDNA was passed through a Chroma-Spin⁺ STE-100 column (Clontech) to remove unreacted primers and cDNA fragments shorter than 100 nucleotides. The olfactory epithelial cDNA population was then subjected to amplification using primers homologous to conserved regions in GPCRs. The first primer set was homologous
 20 to transmembrane segment 2 (TM2) and the second set was homologous to TM 7.5. The TM2 primer set contained 32 oligonucleotides, representing all possible nucleotide sequences capable of encoding the TM2 amino acid sequence motif P-M-Y-F/L-F/Y-F/L, and designed to be non-degenerate at their 3' ends. Sequences of the TM2 primers are as follows:

25

	CCN ATG TAY TTN CTC CTA	SEQ ID NO: 74
	CCN ATG TAY TTN CTC CTC	SEQ ID NO: 75
	CCN ATG TAY TTN CTC CTG	SEQ ID NO: 76
	CCN ATG TAY TTN CTC CTT	SEQ ID NO: 77
30	CCN ATG TAY TTN CTC TTA	SEQ ID NO: 78
	CCN ATG TAY TTN CTC TTC	SEQ ID NO: 79
	CCN ATG TAY TTN CTC TTG	SEQ ID NO: 80
	CCN ATG TAY TTN CTC TTT	SEQ ID NO: 81
	CCN ATG TAY TTN CTT CTA	SEQ ID NO: 82
35	CCN ATG TAY TTN CTT CTC	SEQ ID NO: 83
	CCN ATG TAY TTN CTT CTG	SEQ ID NO: 84

	CCN ATG TAY TTN CTT CTT	SEQ ID NO: 85
	CCN ATG TAY TTN CTT TTA	SEQ ID NO: 86
	CCN ATG TAY TTN CTT TTC	SEQ ID NO: 87
	CCN ATG TAY TTN CTT TTG	SEQ ID NO: 88
5	CCN ATG TAY TTN CTT TTT	SEQ ID NO: 89
	CCN ATG TAY TTN TTC CTA	SEQ ID NO: 90
	CCN ATG TAY TTN TTC CTC	SEQ ID NO: 91
	CCN ATG TAY TTN TTC CTG	SEQ ID NO: 92
	CCN ATG TAY TTN TTC CTT	SEQ ID NO: 93
10	CCN ATG TAY TTN TTC TTA	SEQ ID NO: 94
	CCN ATG TAY TTN TTC TTC	SEQ ID NO: 95
	CCN ATG TAY TTN TTC TTG	SEQ ID NO: 96
	CCN ATG TAY TTN TTC TTT	SEQ ID NO: 97
	CCN ATG TAY TTN TTT CTA	SEQ ID NO: 98
15	CCN ATG TAY TTN TTT CTC	SEQ ID NO: 99
	CCN ATG TAY TTN TTT CTG	SEQ ID NO: 100
	CCN ATG TAY TTN TTT CTT	SEQ ID NO: 101
	CCN ATG TAY TTN TTT TTA	SEQ ID NO: 102
	CCN ATG TAY TTN TTT TTC	SEQ ID NO: 103
20	CCN ATG TAY TTN TTT TTG	SEQ ID NO: 104
	CCN ATG TAY TTN TTT TTT	SEQ ID NO: 105

The TM7.5 primer set was designed to contain the reverse complement of all sequences capable of encoding the TM7.5 amino acid sequence motif P-F/L/I/V-I/V-F/Y-S/T-L. The sequences of the TM7.5 primers are as follows:

	YYTNGTNYTNRYNCYGATANATNATNGGRTT	SEQ ID NO: 106
	YTRTTNCKNAGNWRTANATRAANGGRTT	SEQ ID NO: 107
	TCYTTRTTNCKNAGNGWRTANAYNASNGGRTT	SEQ ID NO: 108
30	TCNTSRTTNCKNARNsARTANATNATNGGRTT	SEQ ID NO: 109
	RTTNCKNARNsWRTANATRAANGGRTT	SEQ ID NO: 110

Reagents and enzymes for amplification were from the Advantage cDNA amplification kit (Clontech). A primary amplification reaction was constructed as follows:

35	5 µl olfactory epithelial cDNA (10-20 µg/ml)
	5 µl 10X PCR reaction buffer (Clontech)
	1 µl TM2 primer set (10 µM)
	1 µl TM7.5 primer set (10 µM)
	1 µl dNTP mix (10 mM each dATP, dCTP, dGTP, dTTP)
40	36 µl PCR-grade H ₂ O
	1 µl Advantage polymerase mix (Clontech)

Amplification was conducted in a PE 480 thermal cycler, using 28 cycles of 95°C for 15 sec, 45°C for 45 sec and 72°C for 2 min. After cycling, the amplification mixture was treated for 1 hour at 37°C with 10 Units of BspEI and 10 Units of PstI restriction enzymes, to degrade non-specific amplification products.

5 The primary amplification products were size-fractionated by agarose gel electrophoresis, and amplification products having a length between 600 and 800 base pairs were selected for secondary amplification.

10 The secondary amplification reaction was conducted identically to the primary amplification reaction, except that the size-selected primary amplification product was used as template. Secondary amplification reactions containing products which generated a specific gel band of between 600 and 800 base pairs were extracted once with phenol/chloroform and once with chloroform, and nucleic acids were precipitated from the reactions by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and
15 resuspended in 15 µl distilled water. After the precipitate dissolved, 3 µl loading dye was added, and the sample was subjected to electrophoresis on a 1.0% low-melting agarose gel containing ethidium bromide. Electrophoresis was conducted at 60V for approximately 40 min, with a 1 kb marker in adjoining lanes.

20 Following electrophoresis, the gel was illuminated with long-wavelength ultraviolet light, and the band was excised from the gel. The gel slice was placed in a 0.5 ml tube, and the tube was heated at 68°C for 15 min. The temperature of the tube was then equilibrated at 45°C. (This is conveniently accomplished in a thermal cycler.) AgarACE™ (Promega) was then added to the tubes, according to the manufacturer's instructions, and incubation at 45°C was continued for 15 min. As a general rule, 2 µl of enzyme per 50 µl of gel slice is
25 adequate. Following AgarACE™ digestion, the digestion mixture was extracted with phenol/chloroform according to the manufacturer's instructions, and nucleic acids were precipitated by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and resuspended in 5 µl distilled water.

30 Gel-purified amplification products were cloned using the TOPO XL PCR Cloning Kit (Invitrogen) according to the manufacturer's instructions. After cloning, individual

colonies were selected at random for nucleotide sequence analysis of the inserts, using procedures for sequence determination that are well-known to those of skill in the art.

Example 2: Use of olfactory receptor polypeptides for screening

5 Components of a scent are identified by determining the interaction between one or more potential odorant molecules and one or more OR polypeptides. For example, if a known original scent involves binding to a particular set of ORs, any subsequent set of molecules which bind to that same set of ORs and stimulate or inhibit the response of the ORs to the same extent as the original scent is capable of re-creating that original scent. If
10 each of the subsequent set of molecules interacts with one and only one OR, then the set of molecules is composed of receptor primary scent components. In similar fashion, scents which involve binding of multiple ORs can be recreated by identifying a molecule, or combination of molecules, which binds to that particular set of ORs.

 Binding of molecules to ORs is determined by a number of methods that are well-
15 known in the art including, but not limited to, in vitro and in silico methods as described herein. Binding of molecules to ORs can also be determined or approximated by using quantitative structure-activity relationships as described herein.

Example 3: Identification of agonists and antagonists of olfactory receptors

20 Interaction of an odorant with a particular OR embedded in the membrane of an olfactory neuron will activate a signaling cascade within the neuron, ultimately resulting in the perception of a particular smell. A molecule, produced for example by combinatorial chemistry, which activates a similar or identical signaling cascade, will induce the perception of the same smell. Such a molecule would be considered a OR agonist. An OR
25 agonist, once identified, can be used as a probe to identify additional agonists, as well as antagonists, of that particular OR.

 Assays for the activation and the end product(s) of signaling cascades are known in the art. For example, direct Ca^{++} imaging can be employed, using either dye -labeled Ca^{++} or dyes that are sensitive to Ca^{++} concentration. Such dyes, and techniques for their use,
30 are available from, for example, Molecular Dynamics (Sunnyvale, CA) and Molecular Probes (Eugene, OR).

Because ORs are transmembrane proteins, identification of agonists and/or antagonists for a particular OR require that the OR is present either in a living cell or in a membrane preparation.

In one embodiment of a method for the determination of OR agonists or antagonists, a known OR agonist is labeled *in situ*, or is resynthesized with an attached label, and is bound to an OR. The effect of various test molecules on the binding of the labeled OR agonist is then determined. Labeling of an OR agonist is accomplished by any of a number of methods that are known to those of skill in the art including, but not limited to, various fluorescent labels (for example, chemical fluorochromes or green fluorescent protein). Binding of the OR agonist is measured by any of a number of competitive binding assays, as are known in the art. A test molecule that displaces the agonist from the OR (*i.e.*, reduces the binding of the agonist) is identified as a candidate agonist or antagonist of the particular OR. In a subsequent experiment, the candidate molecule is bound to the OR, and the effect on the signaling cascade induced by the original agonist is determined. A similar of higher level of activation is indicative of an agonist; while a reduced level of activation of the signaling cascade reflects the action of an antagonist.

In additional embodiments of the displacement assay, an unlabeled agonist is used, and its degree of binding is determined by mass spectrometry. See, for example, U.S. Patent No. 5,894,063; U.S. Patent No. 5,719,060; and Wei *et al.* (1999) *Nature* 399:243-246.

In another embodiment, fluorescent microparticles ("beads"), which can be separated by flow cytometry, are used to identify OR agonists and antagonists. Such beads are available, for example, from Luminex (Austin, TX). Multiple different ORs are attached to the beads, wherein each distinct color of bead is associated with a particular OR. The collection of beads, containing different ORs, is exposed to a test molecule or a collection of test molecules, such as can be synthesized by combinatorial chemistry, and binding of the test molecule(s) is determined, for example, by use of a labeled ligand of the test molecule(s). The beads are sorted according to their color by flow cytometry. Correlation of test molecule binding with bead color allows the determination of test molecules capable of binding to the OR. Agonist or antagonist function of an OR binding molecule is determined by methods described *supra*.

Example 4: Summary of search parameters for homology searches

Step 1: (masking) rempolyatmask raw sequence on -NONE- [?] with remAT_moderate (15) . Continue to step 2.

Step 2: (masking) mask masked sequence from step 1 on RepBase [N] with

5 mask_moderate (85) . Continue to step 3.

Step 3: (masking) mask masked sequence from step 2 on VecBase [N] with mask_moderate (85) . Continue to step 4.

Step 4: blastn masked sequence from step 3 on NR-Nuc [N] with blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 5. Otherwise, stop.

10 Step 5: blastx masked sequence from step 3 on NR-Pro [P] with blastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 6. Otherwise, stop.

Step 6: blastn masked sequence from step 3 on GB_CurAwareness-Nuc [N] with blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 7. Otherwise, stop.

15 Step 7: blastx masked sequence from step 3 on GB_CurAwareness-Pro [P] with blastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 8. Otherwise, stop.

Step 8: tblastx masked sequence from step 3 on NR-Nuc [N] with tblastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 9. Otherwise, stop.

20 Step 9: blastn masked sequence from step 3 on EST [N] with blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 10. Otherwise, stop.

Step 10: blastn masked sequence from step 3 on STS [N] with blastn_10_hits (V=10 B=10) . Stop.

Example 5: Summary of search results

Step	Program	Database	Score	Sequences By Best Hit's Score				No Hits	R	Not un	Finished	Not Run
1	rempolyat mask	NONE-[P]	P/Z/E	0	> 1.0	>= 0	>= 1.0	> 0	74	74	0	0
2	mask	RepBase[N]	P/Z/E	0	> 1.0	>= 0	>= 1.0	> 0	74	74	0	0
3	mask	VecBase[N]	P/Z/E	0	> 1.0	>= 0	>= 1.0	> 0	74	74	0	0
4	blastn	NR-Nuc[N]	P/Z/E	46	< 1.0E-20	<= 28		0	74	0		0
5	blastx	NR-Pro[P]	P/Z/E	16	< 1.0E-20	<= 34		0	50	0		24
6	blastn	GB_CurAwareness-Nuc[N]	P/Z/E	17	< 1.0E-20	<= 31		0	48	0		26
7	blastx	GB_CurAwareness-Pro[P]	P/Z/E	13	< 1.0E-20	<= 28		2	43	0		31
8	tblastx	NR-Nuc[N]	P/Z/E	14	< 1.0E-20	<= 29		0	43	0		31
9	blastn	EST[N]	P/Z/E	10	< 1.0E-20	<= 33		0	43	0		31
10	blastn	STS[N]	P/Z/E	5	< 1.0E-20	<= 33		0	38			

5

Example 6. Datamining and analysis from GenBank

Datamining. A datamining pipeline was built to detect all available OR-like sequences in the public databases and to update the results as new database versions are released. tblastn (Altschul et al., 1997) was used to compare amino acid query sequences to the non-redundant version of GenBank (partitions nt, htg and est_human, all updated to August 6th, 2000), with a non-stringent expectation value cutoff of 1e-4. The queries used included 96 curated OR sequences representing all known families (SEQ ID NO:2651 through SEQ ID NO:2747) and 249 additional HORDE entries (SEQ ID NO:2402 through SEQ ID NO:2650). In a second round 105 newly mined mouse genes (SEQ ID NO:2296 through SEQ ID NO:2401) and 344 newly mined human genes (SEQ ID NO:2009 through SEQ ID NO:2295) were used as additional queries (all datasets are available

electronically). All resulting database entries were catalogued by species and subdivided into four types: mRNA, EST, DNA and genomic, the latter including entries annotated with keyword HTGS_PHASE1-3, or with length at least 10 kb. Low-pass genomic sampling sequences were ignored (keyword HTGS_PHASE0). In addition, a set of 132 olfactory sequence tag (OST) sequences was used. All sequences used were split into contigs according to annotation or, where unavailable, according to runs of at least 50 Ns. All resulting contigs were analyzed for interspersed repeats using RepeatMasker (Smit and Green, 1997). Subcontigs were defined as segments between interspersed repeats, ignoring simple repeats and low-complexity regions.

Localization of genomic clones. The University of Santa Cruz (UCSC) Working Draft Sequence ("golden path", <http://genome.ucsc.edu>) presents a first tentative assembly of the finished and draft human genomic sequence based on the WUSTL clone map (<http://genome.wustl.edu/gsc>). The "golden path" data was used to assign a coordinate to each finished or unfinished genomic clone, in Mb from the p telomere. In parallel, the Unified DataBase (UDB) was used to assign similar Mb coordinates to the clones, based on their marker contents (Chalifa-Caspi et al., 1998). The two maps are largely colinear, and were integrated based on the coordinates of clones that could be localized in both. Clones for which no coordinate could be obtained by either method were assigned a chromosome according to UDB, by sequence similarity to another mapped clone, by annotation, or by e-PCR (Schuler, 1997).

Detection of OR sequences. Each subcontig was compared using FASTY (Pearson et al., 1997) to a curated set of OR protein sequences from several species, yielding a conceptual translation product. The possibility of a pseudogene being disrupted by the insertion of interspersed repeats was taken into account, with the two or more resulting parts being therefore located in different subcontigs. Such compatible candidate sequences were automatically joined into a combined reconstructed pseudogene. Whenever possible, all resulting sequences were trimmed or extended to use a suitable ATG codon for initiation and to end at a stop codon, but avoiding those stop codons that yield products shorter than 275 amino acids. The sequences were finally split into OR or non-OR by comparing them to previously recognized OR sequences and to a non-redundant database of non-OR GPCRs which we extracted from Swiss-Prot. To be automatically classified as an OR, a

new sequence has to be at least 40% identical over at least 100 amino acids to another OR. A more stringent cutoff (50%) was required for shorter sequences.

Definition of OR genes. A given gene could be represented in more than one overlapping genomic clone. Such redundancy was removed by considering two sequences as representing the same gene, if they are in the same chromosome, located in clones less than 300 kb apart and at least 99% identical at the nucleotide level. An exception to this rule is when two genes coappear in the same clone, in which case they were considered to be distinct genes. Sequences localized to a chromosome but without a coordinate were only compared to other sequences within that chromosome, and finally those sequences lacking a chromosomal assignment were compared to the rest, applying only the criterion of sequence similarity. For each resulting gene with more than one constituent sequence, a consensus nucleotide sequence was created after multiple alignment by ClustalW (Higgins et al., 1996) using the fast comparison parameter. This was followed by conceptual translation and end trimming to suitable start and stop codons, as above. Genes with length at least 275 amino acids without frame disruptions (frameshifts, in-frame stop codons or disrupting interspersed repeats) were considered to be full-length and apparently intact. For partial sequences without frame disruptions no statement could be made on their apparent functionality, except when the partial sequences were observed in the genome as such, in which case they were considered to be pseudogenes. Finally, each OR gene was assigned a family and subfamily by amino acid sequence similarity to previously classified OR genes.

The references cited in this example are: Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D. J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25: 3389-402; Chalifa-Caspi, V., Prilusky, J. and Lancet, D. (1998) The Unified Database. Weizmann Institute of Science, Bioinformatics Unit and Genome Center (Rehovot, Israel). World Wide Web URL: bioinformatics.weizmann.ac.il/udb; Higgins, D. G., Thompson, J. D. and Gibson, T. J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol* 266: 383-402; Pearson, W. R., Wood, T., Zhang, Z. and Miller, W. (1997) Comparison of DNA sequences with protein sequences. *Genomics* 46: 24-36; Schuler, G. D. (1997) Sequence mapping by electronic PCR. *Genome Res* 7: 541-50; and Smit, A. F.

A. and Green, P. (1997) RepeatMasker at URL: repeatmasker.genome.washington.edu/cgi-bin/RM2_req.pl.

5 Tables 1 and 2 contain additional information regarding SEQ ID NO. 153 to SEQ ID NO. 1085. The explanation of the entries in Tables 1 and 2 is as follows:

Symbol: The Human Genome Organization gene symbol, as allotted by a procedure to be published soon. OR = Olfactory Receptor, numeral to the immediate right - family designation, capital letters - subfamily designation, rightmost numeral - individual gene within subfamily, n appearing when such number is not assigned yet; P = Pseudogene.

10 All ORs within a family share at least 40% protein sequence identity.

All ORs within a subfamily share at least 60% protein sequence identity.

HORDE: The H serial number within the Human Olfactory Receptor Data Exploratorium (URL bioinfo.weizmann.ac.il/HORDE). The numeral 38 represents the HORDE build (version), gxxx is the individual gene number.

15 Digi: Appearance of a DSnn serial number here means that the sequence has been PCR-amplified from human olfactory epithelial cDNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. See separate page for explanations on the analysis of the DS entries.

OST: OSTnnn is the serial number of the sequence in the Olfactory Sequence Tag collection in the Lancet laboratory (URL bioinfo.weizmann.ac.il/HORDE). Appearance here means that the sequence has been PCR-amplified from human genomic DNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. There are a total of 112 OST sequences.

Trivial name: One or more aliases given to the same gene by different laboratories.
25 Many of the trivial names are of the form ORnn-xx, whereby nn is a chromosome number and xx is an arbitrary numerical identifier.

Tran: (transcribed) Plus appears if the entry was sequenced from cDNA, or was found in the Expressed Sequence Tags (EST) databases. Plus also appears if in the public databases the gene was annotated as mRNA.

30 Int.: (intact) "Yes" indicates that the gene may be intact, as there are no obvious sequence frame disruptions. "Put" (putative) indicates the same, except that the known sequence is short, hence there may be disruptions in the unsequenced segments. "Pol"

indicates a polymorphism between intact and pseudogenic alleles. When no word appears, this indicates a pseudogene.

E: (Extent) FL indicates that the Full Length sequence is known (typically 310 ± 30 amino acids).

5 D: The number of sequence disruptions in the known sequence of a pseudogene.

C: The human chromosomal location of the OR gene, assigned as described under Mb coord.

Mb coord: The location of the OR gene within a human chromosome, in megabase units, beginning at the p-telomere and ending at the q-telomere, computed based on
10 integrating information from Unified Database (URL is bioinfo.weizmann.ac.il/udb) and the University of California Santa Cruz (URL is genome.ucsc.edu).

CDR: The 17 amino acids suggested to line the odorant ligand binding pocket, delineated by the extracellular 2/3 of transmembrane helices 3,4 and 5. The assignment is based on an algorithm at URL
15 bioinformatics.weizman.ac.il/HORDE/humanGenes/CDR.html.

%: (% id) The percent protein identity between the human sequence in the current line and the known rodent (rat or mouse) OR sequence to which it bears the highest similarity.

S: (Species) Rat (R) or mouse (M).

20 Acc: The Genbank accession number of the clone that contains the rodent sequence.

Range: The positions x ... y of the first and last bases within the rodent which constitute the OR coding region. If $x > y$ then the OR is on the reverse strand.

Table 1

25

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
153	OR10D3	H38g001			HSHTPCR09			
154	OR7EnP	H38g002						FL
155	OR1D5	H38g003		OST901	OR17-31	+	pol	FL
156	OR10NnP	H38g00						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
157	OR2F1	H38g00 5		OST902	OLF3;OR7-139;OR7-140	+	yes	FL
158	OR7EnP	H38g00 6						FL
159	OR8FnP	H38g00 7						FL
160	OR2Q1P	H38g00 8			DJ0669B10;OR7-2			FL
161	OR2W1	H38g00 9			AL035402- B;dJ88J8.1;hs6M1-15		yes	FL
162	OR7EnP	H38g01 0				+		FL
163	OR6B1	H38g01 1	DS119		OR7- 3;WUGSC:H_DJ0669B10. 3	+	yes	FL
164	OR10Kn	H38g01 2					yes	FL
165	ORnP	H38g01 3				+		FL
166	OR4F2P	H38g01 4			HS191N21;dJ191N21.4; hs6M1-11			FL
167	OR7EnP	H38g01 5						FL
168	OR1F2P	H38g01 6			OLFMF2	+	yes	FL
169	OR2P1P	H38g01 7			AL035402- A;dJ88J8.2;hs6M1-26			
170	OR7E43P	H38g01 8		OST903	OR4-116			FL
171	OR4F1	H38g01 9			HSDJ0609N19			FL
172	OR7E55P	H38g02 0		OST904	OR2DG;OR3.2			FL
173	OR13Dn	H38g02 1					yes	FL
174	OR4CnP	H38g02 2						FL
175	OR10D1P	H38g02 3		OST074	HSHTPCR03	+		FL
176	OR4Cn	H38g02					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
177	OR8GnP	H38g02 5						
178	OR13CnP	H38g02 6						FL
179	OR4CnP	H38g02 7						FL
180	OR13Cn	H38g02 8					yes	FL
181	OR4CnP	H38g02 9						
182	OR51Bn	H38g03 0					yes	FL
183	OR7E5P	H38g03 1		OST905	OR11-12			FL
184	OR13Cn	H38g03 2					yes	FL
185	OR4Sn	H38g03 3					yes	FL
186	OR51BnP	H38g03 4						FL
187	OR6JnP	H38g03 5						FL
188	OR51Bn	H38g03 6					yes	FL
189	OR7EnP	H38g03 7						FL
190	OR2An	H38g03 8					yes	FL
191	OR7E22P	H38g03 9			OR3.6;OR6DG			FL
192	OR7E4P	H38g04 0			OR11-11a			FL
193	OR7E66P	H38g04 1		OST906	OR3.3;OR3DG;hg630			FL
194	OR6Mn	H38g04 2					yes	FL
195	OR2ALnP	H38g04 3						
196	OR6MnP	H38g04 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
197	OR4D1	H38g04 5			AC005962-A;HSTPCR16	+	yes	FL
198	OR5D2P	H38g04 6		OST907	OR11-7a;OR912-91			FL
199	OR7E38P	H38g04 7		OST127	AC004967	+		FL
200	OR4D2	H38g04 8			AC005962-B		yes	FL
201	OR7E7P	H38g04 9			AC004967-A			FL
202	OR5AHnP	H38g05 0						
203	OR2U2P	H38g05 1			AL050339- B;dJ974I11.2;hs6M1- 23			FL
204	OR2U1P	H38g05 2			974I11;AL050339- C;dJ974I11.3;hs6M1- 24			FL
205	OR2H2	H38g05 3			AC006137- A;dJ271M21.2;hs6M1- 12		yes	FL
206	OR2H5P	H38g05 4		OST616	HS271M21;hs6M1-13			FL
207	OR2In	H38g05 5				+	yes	FL
208	OR11HnP	H38g05 6						FL
209	OR7EnP	H38g05 7				+		
210	OR9In	H38g05 8					yes	FL
211	OR2AFnP	H38g05 9						FL
212	OR13KnP	H38g06 1						FL
213	OR13Cn	H38g06 2					yes	FL
214	OR13Fn	H38g06 3					yes	FL
215	OR9Qn	H38g06 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
216	OR2TnP	H38g06 5						FL
217	OR4Kn	H38g06 6					yes	FL
218	OR2B8P	H38g06 7			dJ313I6.4;hs6M1-29P		yes	FL
219	OR2Tn	H38g06 8					yes	FL
220	OR4Kn	H38g06 9					yes	FL
221	OR2A4	H38g07 0			WUGSC:H_DJ0988G15.2	+	yes	FL
222	OR7EnP	H38g07 1						FL
223	OR4Kn	H38g07 2					yes	FL
224	OR13InP	H38g07 3						FL
225	OR7EnP	H38g07 4						FL
226	OR6Jn	H38g07 5					yes	FL
227	OR4Mn	H38g07 6					yes	FL
228	OR4VnP	H38g07 7						FL
229	OR6Xn	H38g07 8					yes	FL
230	OR51Gn	H38g07 9					yes	FL
231	OR6EnP	H38g08 0						FL
232	OR4NnP	H38g08 1						FL
233	OR6MnP	H38g08 2						FL
234	OR4Nn	H38g08 3					yes	FL
235	OR4Cn	H38g08 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
236	OR4KnP	H38g08 5						FL
237	ORnP	H38g08 6						
238	OR5D3	H38g08 7		OST908	OR11-8b;OR11-8c			
239	OR2G1P	H38g08 8	DS13;D S16	OST619	dJ974I11.4;hs6M1-25	+		FL
240	OR4Kn	H38g08 9					yes	FL
241	OR8BnP	H38g09 0						FL
242	OR2B2	H38g09 1			OR6-1;dJ193B12.4		yes	FL
243	OR7EnP	H38g09 2						FL
244	OR4KnP	H38g09 3						FL
245	OR2AD1P	H38g09 4			dJ25J6.1;hs6M1-8P			FL
246	OR1AAnP	H38g09 5						FL
247	OR1E3P	H38g09 6			OR17-210			FL
248	OR8BnP	H38g09 7						FL
249	OR5Hn	H38g09 8					yes	FL
250	OR1G1	H38g09 9		OST909	OR17-130;OR17-209	+	yes	FL
251	OR5HnP	H38g10 0						FL
252	ORnP	H38g10 1						
253	ORnP	H38g10 2						
254	OR4PnP	H38g10 3						FL
255	OR13Hn	H38g10 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
256	OR7D1P	H38g10 5		OST910	CIT-B-440L2;OR19- 131;OR19-A			FL
257	OR4KnP	H38g10 6						FL
258	OR7E24	H38g10 7		OST911	CIT-B-440L2;OR19-8	+		FL
259	OR51NnP	H38g10 8						FL
260	OR7E18P	H38g10 9		OST912	OR19-14;TPCR26	+		FL
261	OR7E19P	H38g11 0		OST913	HSCIT-B-440L2;OR19- 7;TPCR110	+		FL
262	OR7E41P	H38g11 1		OST914	OR11-20;hg84			FL
263	OR2R1	H38g11 2		OST058				FL
264	OR10ACn P	H38g11 3						FL
265	OR51Ln	H38g11 4					yes	FL
266	OR52JnP	H38g11 5						FL
267	OR9LnP	H38g11 6						
268	OR51PnP	H38g11 7						FL
269	OR5HnP	H38g11 8						FL
270	OR51An	H38g11 9					yes	FL
271	OR5HnP	H38g12 0						FL
272	ORnP	H38g12 1						
273	OR52En	H38g12 2					yes	FL
274	OR5Hn	H38g12 3					yes	FL
275	OR4CnP	H38g12 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
276	OR52En	H38g12 5					yes	FL
277	OR10Dn	H38g12 6					yes	FL
278	OR5HnP	H38g12 7						FL
279	OR13An	H38g12 8					yes	FL
280	OR5HnP	H38g12 9						FL
281	OR5Kn	H38g13 0					yes	FL
282	OR7EnP	H38g13 1						FL
283	OR4DnP	H38g13 2						FL
284	OR2ARnP	H38g13 3						
285	OR7E29P	H38g13 4		OST032				FL
286	OR4CnP	H38g13 5						FL
287	OR5PnP	H38g13 6						FL
288	OR7EnP	H38g13 7						FL
289	OR56An	H38g13 8					yes	FL
290	OR56AnP	H38g13 9						
291	OR5Pn	H38g14 0					yes	FL
292	OR7E53P	H38g14 1		OST915	OR3-142;OR3-143			FL
293	OR5Pn	H38g14 2					yes	FL
294	OR52Ln	H38g14 3					yes	FL
295	OR5E1	H38g14 4			HSTPCR24	+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
296	OR56AnP	H38g14 5						
297	OR4KnP	H38g14 6						
298	OR52Ln	H38g14 7					yes	FL
299	OR7EnP	H38g14 8						
300	OR52XnP	H38g14 9						FL
301	ORnP	H38g15 0						
302	OR56An	H38g15 1					yes	FL
303	OR56AnP	H38g15 2						
304	OR1R1P	H38g15 3			OR17-1			FL
305	OR52EnP	H38g15 4						FL
306	OR51AnP	H38g15 5						FL
307	OR51An	H38g15 6					yes	FL
308	OR4CnP	H38g15 7						FL
309	OR52JnP	H38g15 8						FL
310	OR4RnP	H38g15 9						
311	OR52Jn	H38g16 0					yes	FL
312	OR4CnP	H38g16 1						FL
313	OR51AnP	H38g16 2						FL
314	OR7EnP	H38g16 3						FL
315	OR5MnP	H38g16 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
316	OR10ABn P	H38g16 5						FL
317	OR52SnP	H38g16 6						FL
318	OR5Mn	H38g16 7					yes	FL
319	OR10Sn	H38g16 8					yes	FL
320	OR5MnP	H38g16 9						FL
321	OR10Gn	H38g17 0					yes	FL
322	ORnP	H38g17 1						FL
323	OR5MnP	H38g17 2						FL
324	OR10GnP	H38g17 3						
325	OR10TnP	H38g17 4						FL
326	ORnP	H38g17 5						
327	OR10RnP	H38g17 6						FL
328	OR5MnP	H38g17 7						FL
329	OR7EnP	H38g17 8						FL
330	OR10Tn	H38g17 9					yes	FL
331	OR1E1	H38g18 0	DS37;D S43;DS 46	OST916	HGMP07I;OR17-2;OR17- 32	+	yes	FL
332	OR5BKnP	H38g18 1						
333	OR5MnP	H38g18 2						FL
334	OR3A3	H38g18 3		OST917	OR17-137;OR17- 16;OR17-201	+	yes	FL
335	OR10ADn P	H38g18 4	DS10			+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
336	OR10Rn	H38g18 5				+	yes	FL
337	OR5TnP	H38g18 6						FL
338	OR4GnP	H38g18 7						FL
339	OR6Yn	H38g18 8					yes	FL
340	OR1E2	H38g18 9		OST918	OR17-135;OR17-93	+	yes	FL
341	OR8Hn	H38g19 0					yes	FL
342	OR4Fn	H38g19 1					yes	FL
343	OR10Kn	H38g19 2					yes	FL
344	OR7LnP	H38g19 3						
345	OR8InP	H38g19 4						FL
346	OR10RnP	H38g19 5						
347	OR2AFnP	H38g19 6						FL
348	OR8Kn	H38g19 7					yes	FL
349	ORnP	H38g19 8						
350	OR8KnP	H38g19 9						FL
351	OR5lHn	H38g20 0					yes	FL
352	OR7EnP	H38g20 1						FL
353	ORnP	H38g20 2						
354	OR5BMnP	H38g20 3						FL
355	OR10GnP	H38g20 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
356	OR2Yn	H38g20 5					yes	FL
357	OR10DnP	H38g20 6						FL
358	OR3BnP	H38g20 7						FL
359	OR8Dn	H38g20 8					yes	FL
360	OR5RnP	H38g20 9						
361	OR10Gn	H38g21 0					yes	FL
362	OR5BDnP	H38g21 1						FL
363	OR5ALnP	H38g21 2						FL
364	OR52HnP	H38g21 3						
365	OR10Gn	H38g21 4					yes	FL
366	OR5Mn	H38g21 5					yes	FL
367	OR51Mn	H38g21 6					yes	FL
368	OR6Tn	H38g21 7	DS15;D S146;D S147			+	yes	FL
369	OR6DnP	H38g21 8						FL
370	OR4B1	H38g21 9		OST208			yes	FL
371	OR5ALnP	H38g22 0						FL
372	OR51Qn	H38g22 1					yes	FL
373	OR4Dn	H38g22 2					yes	FL
374	OR52Nn	H38g22 3					yes	FL
375	OR4Xn	H38g22 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
376	OR8Jn	H38g22 5					yes	FL
377	OR51JnP	H38g22 6						FL
378	OR10Gn	H38g22 7					yes	FL
379	OR52En	H38g22 8					yes	FL
380	OR4Xn	H38g22 9					yes	FL
381	OR10A2	H38g23 0	DS5;DS 53;DS5 6	OST363		+		FL
382	OR5Mn	H38g23 1					yes	FL
383	OR52En	H38g23 2					yes	FL
384	OR8Kn	H38g23 3					yes	FL
385	OR10An	H38g23 4	DS55			+	yes	FL
386	OR8LnP	H38g23 5						FL
387	OR5BPnP	H38g23 6						
388	OR52Nn	H38g23 7					yes	FL
389	ORnP	H38g23 8						
390	OR8JnP	H38g23 9						FL
391	OR5Mn	H38g24 0					yes	FL
392	OR52En	H38g24 1					yes	FL
393	OR5Tn	H38g24 2					yes	FL
394	OR52NnP	H38g24 3						FL
395	OR4B2P	H38g24 4		OST919	hg449			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
396	OR51KnP	H38g24 5						FL
397	OR52QnP	H38g24 6						FL
398	OR4Fn	H38g24 7					yes	FL
399	OR11MnP	H38g24 8						
400	OR52Nn	H38g24 9					yes	FL
401	OR56An	H38g25 0					yes	FL
402	OR5AWnP	H38g25 1						FL
403	OR52Nn	H38g25 2					yes	FL
404	ORnP	H38g25 3						
405	OR52EnP	H38g25 4						FL
406	OR5BHnP	H38g25 5						FL
407	OR4QnP	H38g25 6						FL
408	OR51En	H38g25 7					yes	FL
409	OR11KnP	H38g25 8						FL
410	OR12D1P	H38g25 9			AC004174- B;dJ994E9.7;hs6M1-19			FL
411	OR4NnP	H38g26 0				+		FL
412	OR11A1	H38g26 1			AC004174- A;dJ994E9.6;hs6M1-18	+	yes	FL
413	OR10C1	H38g26 2			AC004174;dJ994E9.5;h s6M1-17	+	yes	FL
414	OR2H1	H38g26 3	DS114 ?		OLFR42A-9004-14;OR6- 2;dJ994E9.4;hs6M1-16	+	yes	FL
415	OR9RnP	H38g26 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
416	OR4FnP	H38g26 5						
417	OR7D4	H38g26 6		OST920	OR19-B;hg105			FL
418	OR7E25P	H38g26 7		OST921	CIT-B-440L2;OR19-C			FL
419	OR2D2	H38g26 8			OR11-610		yes	FL
420	OR10An	H38g26 9					yes	FL
421	OR2WnP	H38g27 0				+		
422	OR7E16P	H38g27 1		OST922	CIT-B-440L2;OR19- 133;OR19-9			FL
423	OR52Pn	H38g27 2					yes	FL
424	OR6AnP	H38g27 3						FL
425	OR7D2	H38g27 4	DS70;D S73	OST923	HTPCRHO3;OR19-4	+	yes	FL
426	OR52UnP	H38g27 5						FL
427	OR2AGn	H38g27 6					yes	FL
428	OR7G3	H38g27 7		OST085			yes	FL
429	OR56BnP	H38g27 8						FL
430	OR2AGnP	H38g27 9						FL
431	OR56Bn	H38g28 0					yes	FL
432	OR6AnP	H38g28 1						FL
433	OR4FnP	H38g28 2						FL
434	OR6Wn	H38g28 3					yes	FL
435	OR4Mn	H38g28 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
436	OR52YnP	H38g28 5						
437	OR11HnP	H38g28 6						FL
438	OR9An	H38g28 7					yes	FL
439	OR5Mn	H38g28 8					yes	FL
440	OR6Vn	H38g28 9					yes	FL
441	OR4Nn	H38g29 0				+	yes	FL
442	OR51AnP	H38g29 1						FL
443	OR9PnP	H38g29 2						
444	OR4H6P	H38g29 3			OR15-71;OR15-82			FL
445	OR51FnP	H38g29 4						FL
446	OR7E1P	H38g29 5			AC004923			FL
447	OR51Tn	H38g29 6					yes	FL
448	OR2Vn	H38g29 7					yes	FL
449	OR51HnP	H38g29 8						FL
450	OR51An	H38g29 9					yes	FL
451	OR2AInP	H38g30 0						FL
452	OR2F2	H38g30 1			OR7- 1;WUGSC:H_DJ0669B10. 1		yes	FL
453	OR1F12	H38g30 2			dJ313I6.5;hs6M1-35P		yes	FL
454	OR7G1P	H38g30 3			OR19-15		yes	FL
455	OR7G2	H38g30 4		OST260			yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
456	OR1M1	H38g30 5		OST924	OR19-6		yes	FL
457	OR51UnP	H38g30 6						
458	OR52Hn	H38g30 7					yes	FL
459	OR1F1	H38g30 8		OST925	OLFMP;OR16-36;OR16- 37;OR16-88;OR16- 89;OR16-90	+	yes	FL
460	OR10PnP	H38g30 9						
461	OR4FnP	H38g31 0						FL
462	OR2T1	H38g31 1			OR1-25		yes	FL
463	OR7EnP	H38g31 2						FL
464	OR51Gn	H38g31 3					yes	FL
465	OR2Tn	H38g31 4					yes	FL
466	OR5BGnP	H38g31 5						
467	OR5WnP	H38g31 6						FL
468	OR51Sn	H38g31 7					yes	FL
469	OR5WnP	H38g31 8						
470	OR51AnP	H38g31 9						FL
471	OR5Dn	H38g32 0					yes	FL
472	OR7EnP	H38g32 1						FL
473	OR51Fn	H38g32 2					yes	FL
474	OR5Dn	H38g32 3					yes	FL
475	OR52Rn	H38g32 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int .	E
476	ORnP	H38g32 5						FL
477	OR7EnP	H38g32 6						FL
478	OR6Qn	H38g32 7					yes	FL
479	OR4Fn	H38g32 8					yes	FL
480	OR7EnP	H38g32 9						
481	OR7En	H38g33 0					yes	FL
482	OR4Nn	H38g33 1					yes	FL
483	OR2ASnP	H38g33 2						
484	OR11Hn	H38g33 3					yes	FL
485	OR2Tn	H38g33 4					yes	FL
486	OR2TnP	H38g33 5						
487	OR2AKnP	H38g33 6						FL
488	ORnP	H38g33 7						
489	OR5DnP	H38g33 8						FL
490	OR7EnP	H38g33 9						
491	OR5L2	H38g34 0			HSHTPCRXL6	+	yes	FL
492	OR5Dn	H38g34 1					yes	FL
493	ORnP	H38g34 2						
494	OR10Qn	H38g34 3					yes	FL
495	OR9MnP	H38g34 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
496	OR7E62P	H38g34 5		OST926	OR2-4;OR2-52;OR2- 53;OR2-75			FL
497	OR9LnP	H38g34 6						FL
498	OR7E46P	H38g34 7		OST379				FL
499	OR1S1	H38g34 8		OST034			yes	FL
500	OR5DnP	H38g34 9						
501	OR9InP	H38g35 0						FL
502	OR5Dn	H38g35 1					yes	FL
503	OR9QnP	H38g35 2						FL
504	OR51CnP	H38g35 3						
505	OR5WnP	H38g35 4						
506	OR9InP	H38g35 5						FL
507	OR51AnP	H38g35 6						FL
508	OR5L1	H38g35 7		OST262			yes	FL
509	OR7EnP	H38g35 8				+		
510	OR5BLnP	H38g35 9						
511	OR51En	H38g36 0					yes	FL
512	OR51Dn	H38g36 1					yes	FL
513	OR52In	H38g36 2					yes	FL
514	OR4KnP	H38g36 3	DS67			+		FL
515	OR52In	H38g36 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
516	OR4KnP	H38g36 5						FL
517	OR52MnP	H38g36 6						FL
518	ORnP	H38g36 7						
519	ORnP	H38g36 8						
520	ORnP	H38g36 9						FL
521	ORnP	H38g37 0						
522	ORnP	H38g37 1						
523	ORnP	H38g37 2						
524	ORnP	H38g37 3						
525	ORnP	H38g37 4						
526	OR6Pn	H38g37 5					yes	FL
527	OR7EnP	H38g37 6						FL
528	ORnP	H38g37 7						
529	OR7EnP	H38g37 8						FL
530	ORnP	H38g37 9						
531	OR10XnP	H38g38 0						FL
532	OR10Zn	H38g38 1					yes	FL
533	OR6KnP	H38g38 2						FL
534	OR6Kn	H38g38 3					yes	FL
535	OR1FnP	H38g38 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
536	OR1ABnP	H38g38 5						
537	OR52MnP	H38g38 6						FL
538	OR1XnP	H38g38 7						FL
539	OR4FnP	H38g38 8						
540	OR52MnP	H38g38 9						FL
541	OR2Vn	H38g39 0					yes	FL
542	OR2V1P	H38g39 1		OST265				FL
543	OR2Zn	H38g39 2					yes	FL
544	OR52KnP	H38g39 3				+		
545	OR10Hn	H38g39 4					yes	FL
546	OR2Dn	H38g39 5					yes	FL
547	OR7EnP	H38g39 6						
548	OR11GnP	H38g39 7						FL
549	ORnP	H38g39 8						
550	OR11Gn	H38g39 9					yes	FL
551	OR11HnP	H38g40 0						FL
552	OR6Kn	H38g40 1					yes	FL
553	OR11Hn	H38g40 2					yes	FL
554	OR6KnP	H38g40 3						
555	OR11HnP	H38g40 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
556	OR6KnP	H38g40 5						FL
557	OR6Kn	H38g40 6					yes	FL
558	OR2Ln	H38g40 7					yes	FL
559	OR4GnP	H38g40 8						
560	OR6Nn	H38g40 9					yes	FL
561	OR2LnP	H38g41 0						
562	OR9A1	H38g41 1			HSHTPCR06			
563	OR6Nn	H38g41 2					yes	FL
564	OR10Hn	H38g41 3					yes	FL
565	OR7EnP	H38g41 4						FL
566	OR2AQnP	H38g41 5						
567	OR2LnP	H38g41 6						FL
568	OR5ARn	H38g41 7					yes	FL
569	OR7EnP	H38g41 8						FL
570	OR10AA P	H38g41 9						FL
571	OR10JnP	H38g42 0						FL
572	OR5A1P	H38g42 1	DS69;D S71;DS 128;DS 129	OST181		+	yes	FL
573	OR2AHnP	H38g42 2						FL
574	OR10JnP	H38g42 3						FL
575	OR56BnP	H38g42						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
576	OR5M1	H38g42 5		OST050			yes	FL
577	OR52WnP	H38g42 6						
578	OR5AMnP	H38g42 7						FL
579	OR52BnP	H38g42 8						FL
580	OR5MnP	H38g42 9						FL
581	OR5APnP	H38g43 0						FL
582	OR56Bn	H38g43 1					yes	FL
583	OR5APn	H38g43 2					yes	FL
584	OR52Bn	H38g43 3					yes	FL
585	OR9Gn	H38g43 4					yes	FL
586	OR52Kn	H38g43 5					yes	FL
587	OR5MnP	H38g43 6						FL
588	OR52Kn	H38g43 7					yes	FL
589	OR52KnP	H38g43 8				+		FL
590	OR52BnP	H38g43 9						FL
591	OR2B6P	H38g44 0			OR6-31		yes	FL
592	OR2WnP	H38g44 1						FL
593	OR2AnP	H38g44 2						FL
594	ORnP	H38g44 3						
595	OR2LnP	H38g44 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
596	OR2W2P	H38g44 5	DS148		dJ313I6.2;hs6M1-30P	+		FL
597	OR2LnP	H38g44 6						
598	OR2B7P	H38g44 7			dJ313I6.3;hs6M1-31P			FL
599	OR2Ln	H38g44 8					yes	FL
600	OR5BFn	H38g44 9					yes	FL
601	OR2LnP	H38g45 0						FL
602	OR7EnP	H38g45 1						
603	OR1H1	H38g45 2	DS122	OST26		+		FL
604	ORnP	H38g45 3						
605	OR4Dn	H38g45 4					yes	FL
606	OR1Ln	H38g45 5					yes	FL
607	OR5AXn	H38g45 6					yes	FL
608	OR5An	H38g45 7					yes	FL
609	OR5AYn	H38g45 8					yes	FL
610	OR13Gn	H38g45 9					yes	FL
611	OR5BBnP	H38g46 0						
612	OR9GnP	H38g46 1						FL
613	OR2TnP	H38g46 2						FL
614	ORnP	H38g46 3						FL
615	OR1Jn	H38g46 4				+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
616	OR2CnP	H38g46 5						FL
617	OR9GnP	H38g46 6						FL
618	OR2C1	H38g46 7			OLFmf3	+	yes	FL
619	OR51AnP	H38g46 8						
620	OR9Gn	H38g46 9					yes	FL
621	OR52Bn	H38g47 0					yes	FL
622	OR1K1	H38g47 1			hg99		yes	FL
623	OR51RnP	H38g47 2						FL
624	OR7EnP	H38g47 3						FL
625	OR52PnP	H38g47 4						FL
626	OR7EnP	H38g47 5						FL
627	OR7EnP	H38g47 6						
628	OR4KnP	H38g47 7	DS66		OR21-1	+		FL
629	OR4KnP	H38g47 8			OR21-2			FL
630	OR7EnP	H38g47 9						
631	OR51In	H38g48 0					yes	FL
632	OR51In	H38g48 1					yes	FL
633	OR2AnP	H38g48 2						
634	OR2A2	H38g48 3		OST008				FL
635	OR2AnP	H38g48 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
636	OR2Gn	H38g48 5					yes	FL
637	OR2AnP	H38g48 6						
638	OR6Fn	H38g48 7	DS20;D S21;DS 23;DS2 7;DS28 ;DS39; DS40;D S113;D S126;D S135;D S137;D S138;D S139;D S140;D S141;D S145			+	yes	FL
639	OR2AnP	H38g48 8						
640	OR2Gn	H38g48 9					yes	FL
641	OR7E37P	H38g49 0			hg533	+		FL
642	OR5AVn	H38g49 1	DS4;DS 6;DS11			+	yes	FL
643	OR2AJnP	H38g49 2						FL
644	OR13EnP	H38g49 3						FL
645	OR2Cn	H38g49 4					yes	FL
646	OR2TnP	H38g49 5						
647	OR2WnP	H38g49 6						
648	OR13Jn	H38g49 7					yes	FL
649	OR6RnP	H38g49 8						FL
650	OR5ATn	H38g49 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
651	OR2Zn	H38g50 0					yes	FL
652	OR4Ln	H38g50 1					yes	FL
653	OR4UnP	H38g50 2						FL
654	OR4Fn	H38g50 3					yes	FL
655	OR4FnP	H38g50 4						FL
656	OR4Fn	H38g50 5					yes	FL
657	OR4Fn	H38g50 6					yes	FL
658	OR4AnP	H38g50 7						FL
659	OR4LnP	H38g50 8						FL
660	OR7E33P	H38g50 9		OST927	hg688			FL
661	OR2Cn	H38g51 0					yes	FL
662	OR4Kn	H38g51 1					yes	FL
663	OR5U1	H38g51 2			bA150A6.4;hs6M1-28		yes	FL
664	OR4Kn	H38g51 3					yes	FL
665	OR5V1	H38g51 4			bA150A6.2;hs6M1-21		yes	FL
666	OR4QnP	H38g51 5						FL
667	OR12D3	H38g51 6			bA150A6.1;hs6M1-27		yes	FL
668	OR4Kn	H38g51 7					yes	FL
669	OR51CnP	H38g51 8						
670	OR1J2	H38g51 9		OST044	hg152		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
671	OR5BJnP	H38g52 0						
672	OR1J1	H38g52 1	DS130	OST928	hg32	+	yes	FL
673	OR13En	H38g52 2					put	
674	OR4KnP	H38g52 3	DS1			+		FL
675	OR1LnP	H38g52 4						
676	OR2CnP	H38g52 5						
677	OR4TnP	H38g52 6						FL
678	OR5BnP	H38g52 7						
679	OR4Kn	H38g52 8					yes	FL
680	OR11Ln	H38g52 9					yes	FL
681	OR7E68P	H38g53 0		OST929	OR912-108;OR912- 109;OR912-110;OR912- 46;hg523;hg674			FL
682	OR7EnP	H38g53 1						FL
683	OR7E31P	H38g53 2		OST016;O ST205				FL
684	OR7EnP	H38g53 3						FL
685	OR5AKnP	H38g53 4						FL
686	OR5AKn	H38g53 5					yes	FL
687	OR5AKn	H38g53 6					yes	FL
688	OR5BQnP	H38g53 7						
689	OR1Nn	H38g53 8	DS136; DS142			+	yes	FL
690	OR1J4	H38g53 9		OST930	HSHTPCR01	+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
691	OR1Nn	H38g54 0					yes	FL
692	OR2AnP	H38g54 1						FL
693	OR2ANnP	H38g54 2						
694	OR5K1	H38g54 3			HSHTPCR10	+	yes	FL
695	OR2K2	H38g54 4			HSHTPCR06		yes	FL
696	OR8Hn	H38g54 5					yes	FL
697	ORnP	H38g54 6						
698	OR4AnP	H38g54 7						
699	OR4An	H38g54 8					yes	FL
700	OR6Sn	H38g54 9					yes	FL
701	OR4RnP	H38g55 0						
702	OR13Cn	H38g55 1					yes	FL
703	OR13DnP	H38g55 2						FL
704	OR7EnP	H38g55 3						FL
705	OR10PnP	H38g55 4						FL
706	OR8In	H38g55 5					yes	FL
707	OR8G1	H38g55 6			HSTPCR25	+	put	
708	ORnP	H38g55 7						
709	OR5F1	H38g55 8			OR11-10		yes	FL
710	OR5FnP	H38g55 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
711	OR6BnP	H38g56 0						FL
712	OR2D1	H38g56 1			hg27		put	
713	OR5ASn	H38g56 2					yes	FL
714	OR5SnP	H38g56 3						FL
715	OR5AQnP	H38g56 4						
716	OR6BnP	H38g56 5						FL
717	OR5JnP	H38g56 6						FL
718	OR9AnP	H38g56 7						FL
719	OR5BEnP	H38g56 8						FL
720	OR9An	H38g56 9					yes	FL
721	OR8Hn	H38g57 0					yes	FL
722	OR5BNnP	H38g57 1						
723	OR8Jn	H38g57 2					yes	FL
724	OR9NnP	H38g57 3						
725	OR7EnP	H38g57 4						FL
726	OR7E9P	H38g57 5		OST289				FL
727	OR8KnP	H38g57 6						
728	OR2AnP	H38g57 7						
729	OR8Kn	H38g57 8					yes	FL
730	OR7E39P	H38g57 9		OST931	hg611			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
731	OR7E27P	H38g58 0		OST932	hg616			
732	OR2Hn	H38g58 1					put	
733	OR13CnP	H38g58 2						FL
734	OR13Cn	H38g58 3					yes	FL
735	OR2S1P	H38g58 4		OST611				FL
736	OR2AMnP	H38g58 5						
737	OR1N1	H38g58 6		OST933	OR1-26		put	
738	OR2S2	H38g58 7		OST715			yes	FL
739	OR7E26P	H38g58 8			OR1-51;OR1-72;OR1-73;OR912-95			
740	OR1F11	H38g58 9			hg91		put	
741	OR5ACnP	H38g59 0						FL
742	OR5B10P	H38g59 1			OR13-34;OR13-64;OR13-67			
743	OR2AnP	H38g59 2						FL
744	OR1E5	H38g59 3	DS117; DS143		OR13-66	+	put	
745	OR4Fn	H38g59 4					yes	FL
746	OR5CnP	H38g59 5						
747	OR2WnP	H38g59 6						
748	OR2L2	H38g59 7			HSHTPCRHO7	+	put	
749	OR4H8P	H38g59 8			OR14-58			
750	OR5D10P	H38g59 9			OR912-94			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
751	OR7A12P	H38g60 0			OR14-11;OR14-59			
752	OR2L1	H38g60 1			HSHTPCR02	+	put	
753	OR2F3P	H38g60 2			OR14-60		put	
754	OR4H10P	H38g60 3		OST934	OR15-69;OR15- 80;OR15-81			
755	OR5H1	H38g60 4			HSHTPCR14	+	put	
756	OR2K1	H38g60 5			HSHTPCR17	+	put	
757	OR7E11P	H38g60 6			OR11-2			
758	OR7A3P	H38g60 7		OST935	OR11-7b			
759	OR6A1	H38g60 8			OR11-55	+	yes	FL
760	OR5I1	H38g60 9			OLF1	+	yes	FL
761	OR2H3	H38g61 0			HUMORLMHC	+	yes	FL
762	OR10J1	H38g61 1	DS3;DS 14		HSHGMP07J	+	yes	FL
763	OR7E3P	H38g61 2			OR11-9			
764	OR1D6P	H38g61 3			OR11-13;OR11-22			
765	OR5D10P	H38g61 4			OR18-17;OR18- 42;OR18-43;OR18-44			
766	OR5D5P	H38g61 5			OR18-79;OR912-47			
767	OR52A1	H38g61 6			HPFH1OR	+	yes	FL
768	OR2AEn	H38g61 7					yes	FL
769	OR6LnP	H38g61 8						FL
770	OR6LnP	H38g61 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
771	OR7MnP	H38g62 0						
772	OR13Cn	H38g62 1					yes	FL
773	OR13Cn	H38g62 2					yes	FL
774	OR2InP	H38g62 3				+		
775	OR4An	H38g62 4					yes	FL
776	OR2InP	H38g62 5				+		
777	OR4AnP	H38g62 6						FL
778	OR4AnP	H38g62 7						FL
779	OR8C1P	H38g62 8			OR11-175			
780	OR4AnP	H38g62 9						FL
781	OR7E15P	H38g63 0			OR11-392			
782	OR10A1	H38g63 2			OR11-403		put	
783	OR2An	H38g63 3				+	put	
784	OR7EnP	H38g63 4				+		FL
785	OR7En	H38g63 5				+	put	
786	OR51A1P	H38g63 6			HPFH6OR	+		FL
787	OR7E47P	H38g63 7			HSORBPL41;bpl41-16	+		FL
788	OR5B5P	H38g63 8			OR3-144;OR912-92			
789	OR1F10	H38g63 9			OR3-145		put	
790	OR8G2	H38g64 0			HSTPCR120	+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
791	OR1Sn	H38g64 1					yes	FL
792	OR4AnP	H38g64 2						FL
793	OR4AnP	H38g64 3						FL
794	OR4AnP	H38g64 4						FL
795	OR4AnP	H38g64 5						FL
796	OR4AnP	H38g64 6						FL
797	OR4AnP	H38g64 7						FL
798	OR4An	H38g64 8					yes	FL
799	OR4An	H38g64 9					yes	FL
800	OR7E42P	H38g65 0		OST001				
801	OR2M3P	H38g65 1		OST003				
802	OR4H11P	H38g65 2			OR4-114;OR4-115;OR4- 119			
803	OR7E57P	H38g65 3		OST007				
804	OR2B1P	H38g65 4			OR5-40;OR5-41		put	
805	OR7E34P	H38g65 5		OST011				
806	OR7E56P	H38g65 6		OST013				
807	OR3AnP	H38g65 7						
808	OR4H5P	H38g65 8			OR5-39;OR5-84			
809	OR1En	H38g65 9	DS47;D S115;D S120;D S121;D S123;D			+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int .	E
			S125					
810	OR51CnP	H38g66 0						
811	OR2WnP	H38g66 1						FL
812	OR51B1P	H38g66 2			AF149710			FL
813	OR7E81P	H38g66 3		OST021				
814	OR7E44P	H38g66 4		OST022				
815	OR5B7P	H38g66 5			OR6-55;OR6-57			
816	OR7E36P	H38g66 6		OST024				
817	OR2A5	H38g66 7			OR7-138;OR7-141		put	
818	OR5B1P	H38g66 8		OST936	OR8-122;OR8-123			
819	OR8B8	H38g66 9			HSTPCR85	+	yes	FL
820	OR8B4P	H38g67 0			AC002556-D		yes	FL
821	ORnP	H38g67 1						FL
822	OR8B3	H38g67 2			AC002556-B		yes	FL
823	OR2Bn	H38g67 3					yes	FL
824	OR8B6P	H38g67 4			AC002556-G			FL
825	OR8B5P	H38g67 5			AC002556-A			FL
826	OR4E2	H38g67 6			AE000658-A		yes	FL
827	OR8B7P	H38g67 7			AC002556-F			FL
828	OR11JnP	H38g67 8						FL
829	OR4E1P	H38g67 9			AE000658			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
830	OR10DnP	H38g68 0						
831	ORnP	H38g68 1						
832	OR8D2	H38g68 2			AC002556-E		yes	FL
833	OR11InP	H38g68 3						FL
834	OR11JnP	H38g68 4						FL
835	OR10AnP	H38g68 5	DS12;D S65			+		FL
836	OR8C3P	H38g68 6			OR912-106;OR912- 45;pDJ9j14			FL
837	OR2DnP	H38g68 7						FL
838	OR4PnP	H38g68 8						
839	OR7E21P	H38g68 9		OST035	OR4DG			
840	OR2M1	H38g69 0		OST037			put	
841	OR7AnP	H38g69 1						
842	OR5D11P	H38g69 2			OR8-125;OR8-127			
843	OR7E50P	H38g69 3			OR8-126			
844	OR7E45P	H38g69 4		OST049				
845	OR7E77P	H38g69 5		OST060				
846	OR8B2	H38g69 6			AC002556-C		yes	FL
847	OR8D1	H38g69 7		OST004	pDJ9j14		yes	FL
848	OR8B1P	H38g69 8		OST937	OR11-561			FL
849	OR7A1P	H38g69 9		OST938	OLF4p;OR19-3;hg513			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
850	OR7E8P	H38g70 0			OR11-11a;pDJ392a17			FL
851	OR4DnP	H38g70 1						FL
852	OR7E80P	H38g70 2		OST939	pDJ392a17			FL
853	OR4DnP	H38g70 3						FL
854	OR7E10P	H38g70 4			AC000385-A			FL
855	OR10B1P	H38g70 5			AC003956-A;OR19-19			FL
856	OR2InP	H38g70 6				+		
857	OR4Dn	H38g70 7					yes	FL
858	OR5ACn	H38g70 8					put	
859	OR2I1	H38g70 9			AC004179- A;dJ271M21.7;hs6M1- 14	+		
860	OR10H1	H38g71 0			AC004510	+	yes	FL
861	OR7E59P	H38g71 1		OST119				
862	OR7E28P	H38g71 2		OST128				
863	OR5B3	H38g71 3		OST129			put	
864	OR2A6	H38g71 4		OST182			put	
865	OR6Cn	H38g71 5					put	
866	OR7E54P	H38g71 6		OST185				
867	OR7E48P	H38g71 7		OST193				
868	OR67AnP	H38g71 8						FL
869	OR4DnP	H38g71 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
870	OR4CnP	H38g72 0						FL
871	OR4DnP	H38g72 1						FL
872	OR10H2	H38g72 2			AC004597-A	+	yes	FL
873	OR10H3	H38g72 3			AC004597-B	+	yes	FL
874	OR55CnP	H38g72 4						
875	OR55BnP	H38g72 5						
876	OR52VnP	H38g72 6						FL
877	OR2B3	H38g72 7			OR6- 4;dJ80I19.1;hs6M1-1		yes	FL
878	OR52TnP	H38g72 8						FL
879	OR2J1P	H38g72 9			OR6- 5;dJ80I19.2;hs6M1-4			FL
880	OR52HnP	H38g73 0						FL
881	OR2J3	H38g73 1			OR6- 6;dJ80I19.7;hs6M1-3		yes	FL
882	OR52An	H38g73 2				+	put	
883	OR4Qn	H38g73 3					put	
884	OR52BnP	H38g73 4						FL
885	OR2N1P	H38g73 5	DS9		OR6- 7;dJ80I19.3;hs6M1-2	+		FL
886	OR51EnP	H38g73 6				+		
887	OR2J2	H38g73 7			OR6- 8;dJ80I19.4;hs6M1-6		yes	FL
888	OR2In	H38g73 8				+	put	
889	OR2J4P	H38g73 9			OR6- 9;dJ80I19.5;hs6M1-5			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
890	OR7E40P	H38g74 0		OST215				
891	OR2H4P	H38g74 1			OR6- 3;dJ80I19.6;hs6M1-7			FL
892	OR7E52P	H38g74 2		OST245				
893	OR2InP	H38g74 3				+		
894	OR6C1	H38g74 4		OST267			put	
895	OR7E30P	H38g74 5		OST339				
896	OR5BAnP	H38g74 6	DS132			+		
897	OR7H1P	H38g74 7		OST940	CIT-B-440L2			FL
898	OR5B2	H38g74 8		OST073			yes	FL
899	OR5AZnP	H38g74 9						FL
900	OR5Bn	H38g75 0					yes	FL
901	OR52Bn	H38g75 1					yes	FL
902	OR5BnP	H38g75 2						FL
903	OR52Dn	H38g75 3					yes	FL
904	OR7A11	H38g75 4		OST527	CIT-HSP-87m17			FL
905	OR5BnP	H38g75 5						FL
906	OR51AnP	H38g75 6						FL
907	OR7A15P	H38g75 7		OST941	CIT-HSP-87m17;OR19- 1;OR19-134;OR19-146			FL
908	OR7C2	H38g75 8			CIT-HSP-87m17;OR19- 18		yes	FL
909	OR7E23P	H38g75 9		OST942	OR21-3			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
910	OR2E1	H38g76 0			HS29K1;HSNH0569I24;h s6M1-9			
911	OR1I1	H38g76 1			F20569;OR19-20		yes	FL
912	OR1RnP	H38g76 2						FL
913	OR4F3	H38g76 3			AC004908		yes	FL
914	OR2AEn	H38g76 4					yes	FL
915	OR2InP	H38g76 5				+		
916	OR52AnP	H38g76 6				+		
917	OR7C1	H38g76 7		OST943	CIT-HSP-146e8;OR19- 5;TPCR86	+	yes	FL
918	OR2A3P	H38g76 8			AC004889-B			FL
919	OR7A5	H38g76 9	DS8;DS 19;DS6 1;DS68 ;DS112	OST944	HTPCR2	+	yes	FL
920	OR2InP	H38g77 0	DS72			+		
921	OR7A10	H38g77 1		OST027	CIT-HSP-146e8		yes	FL
922	OR2An	H38g77 2				+	put	
923	OR2M2	H38g77 3		OST423			put	
924	OR7A8P	H38g77 4		OST042	OR19-11;hg83			FL
925	OR2An	H38g77 5				+	put	
926	OR7E20P	H38g77 6		OST516				
927	OR2AnP	H38g77 7				+		
928	OR5BHnP	H38g77 8				+		
929	OR1En	H38g77					put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
930	OR1EnP	H38g78 0						
931	OR5Bn	H38g78 1					yes	FL
932	OR8RnP	H38g78 2						
933	OR5ANn	H38g78 3					yes	FL
934	OR5ANnP	H38g78 4						FL
935	OR5BRnP	H38g78 5						FL
936	OR2A1	H38g78 6			AC004889-A	+	yes	FL
937	OR10An	H38g78 7					yes	FL
938	OR2A9	H38g78 8	DS149		HSDJ0798C17	+		FL
939	OR2A7	H38g78 9			HSDJ0798C17	+	yes	FL
940	OR10A3	H38g79 0			HSHTPCR12	+	yes	FL
941	OR10Cn	H38g79 1					yes	FL
942	OR7A2P	H38g79 2			OLF4p;OR19-18;hg1003		yes	FL
943	OR10WnP	H38g79 3						FL
944	OR7A17	H38g79 4			HSHTPCR19		yes	FL
945	OR5Bn	H38g79 5					yes	FL
946	OR5BnP	H38g79 6						FL
947	OR1Q1	H38g79 7		OST226	HSTPCR106;OR9-A;hrPK-465_F_21	+	yes	FL
948	OR2Hn	H38g79 8	DS133; DS144; DS150			+	yes	FL
949	OR7EnP	H38g79						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
950	OR7A14	H38g80 0		OST945	OR19-12			
951	OR1B1	H38g80 1			OR9-B;hRPK-465_F_21		yes	FL
952	OR12D2	H38g80 2			AC004171;dJ994E9.8;h s6M1-20	+	yes	FL
953	OR7EnP	H38g80 3						FL
954	OR8BnP	H38g80 4						FL
955	OR1L1	H38g80 5			OR9-C;hRPK- 465_F_21;hg23		yes	FL
956	OR11An	H38g80 6					yes	FL
957	OR7AnP	H38g80 7						
958	OR1C1	H38g80 8			HSTPCR27	+	yes	FL
959	OR1D2	H38g80 9		OST946	OR17-4	+	yes	FL
960	OR1L3	H38g81 0			OR9-D;hRPK-465_F_21		yes	FL
961	OR12DnP	H38g81 1						FL
962	OR4G1P	H38g81 2			OLB			FL
963	OR2B4P	H38g81 3			AL050339- A;dJ974I11.1;hs6M1- 22			
964	OR11H1	H38g81 4			OR22-1		yes	FL
965	OR4Fn	H38g81 5					yes	FL
966	OR56AnP	H38g81 6						FL
967	OR8NnP	H38g81 7						FL
968	OR7EnP	H38g81 8						
969	OR4Pn	H38g81					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
970	OR6Cn	H38g82 0					put	
971	OR5BCnP	H38g82 1						
972	OR10QnP	H38g82 2	DS64			+		FL
973	OR5BnP	H38g82 3						FL
974	OR10PnP	H38g82 4						FL
975	OR1L4	H38g82 5		OST046	OR9-E;hRPK-465_F_21		yes	FL
976	OR2APnP	H38g82 6						
977	OR1L6	H38g82 7		OST947	HShRPK-465_F_21;hg16		yes	FL
978	OR6UnP	H38g82 8						FL
979	OR5C1	H38g82 9			OR9-F;hRPK-465_F_21		yes	FL
980	OR11InP	H38g83 0						FL
981	OR4AnP	H38g83 1						FL
982	OR4GnP	H38g83 2						FL
983	OR10Vn	H38g83 3					yes	FL
984	OR4G2P	H38g83 4			HS14a-1-B			FL
985	OR10VnP	H38g83 5				+		
986	OR4F4	H38g83 6			HS14a-1-A		yes	FL
987	OR4G3P	H38g83 7			OLC-7501			FL
988	OR5AKnP	H38g83 8						FL
989	OR10YnP	H38g83 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
990	OR4GnP	H38g84 0						FL
991	ORnP	H38g84 1						
992	OR4Fn	H38g84 2					yes	FL
993	OR8A1	H38g84 3		OST025			yes	FL
994	OR8Bn	H38g84 4					yes	FL
995	OR6DnP	H38g84 5						
996	OR7E14P	H38g84 6		OST948	OR11-5	+		FL
997	OR2M4	H38g84 7		OST710	HSHTPCR18	+	put	
998	OR4WnP	H38g84 8						
999	OR4Fn	H38g84 9	DS36			+	yes	FL
1000	OR7EnP	H38g85 0						
1001	OR4GnP	H38g85 1						FL
1002	OR10JnP	H38g85 2						
1003	OR52En	H38g85 3					yes	FL
1004	OR4RnP	H38g85 4						FL
1005	OR4Cn	H38g85 5					yes	FL
1006	OR4AnP	H38g85 6						
1007	OR4AnP	H38g85 7	DS54			+		
1008	OR4AnP	H38g85 8						FL
1009	OR9Gn	H38g85 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1010	OR10An	H38g86 0					yes	FL
1011	OR4Cn	H38g86 1					yes	FL
1012	OR10VnP	H38g86 2						
1013	OR10UnP	H38g86 3						FL
1014	OR7E2P	H38g86 4	DS127		OR11-6;hg94	+		FL
1015	OR7E35P	H38g86 5		OST018				FL
1016	OR9KnP	H38g86 6						
1017	OR7E13P	H38g86 7		OST949	OR11-4			FL
1018	OR7EnP	H38g86 8						FL
1019	OR9Kn	H38g86 9					yes	FL
1020	ORnP	H38g87 0						FL
1021	OR7EnP	H38g87 1		OST950	OR11-1;hg500	+		FL
1022	OR7EnP	H38g87 2						FL
1023	OR3A4P	H38g87 3		OST951	OR17-24;OR17-25	+	yes	FL
1024	OR8QnP	H38g87 4						
1025	OR7EnP	H38g87 5						FL
1026	OR7EnP	H38g87 6						FL
1027	OR3A1	H38g87 7	DS2		OLFRA03;OR17- 40;hg138	+	yes	FL
1028	OR5Gn	H38g87 8					yes	FL
1029	OR5MnP	H38g87 9						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1030	OR7EnP	H38g88 0						FL
1031	OR5G1P	H38g88 1		OST952	OR11- 104;OR93;OR93Hum			FL
1032	OR5PnP	H38g88 2						FL
1033	OR10AEn P	H38g88 3						
1034	OR3A2	H38g88 4		OST953	OR17-228	+	yes	FL
1035	OR10Jn	H38g88 5					yes	FL
1036	OR1D3P	H38g88 6		OST954	OR17-23			FL
1037	OR10Jn	H38g88 7					yes	FL
1038	OR1D4	H38g88 8			OR17-30	+	yes	FL
1039	OR5GnP	H38g88 9						FL
1040	OR4SnP	H38g89 0						FL
1041	OR5GnP	H38g89 1						FL
1042	OR9HnP	H38g89 2						FL
1043	OR1A1	H38g89 3			OR17-7	+	yes	FL
1044	OR1A2	H38g89 4			OR17-6	+	yes	FL
1045	OR8AnP	H38g89 5						FL
1046	OR1P1P	H38g89 6			OR17-208	+		FL
1047	OR7E12P	H38g89 7		OST955	AC000378-A;OR11- 3;hg1058	+		FL
1048	OR4A1P	H38g89 8			OR11-30			FL
1049	OR10G3	H38g89 9			AE000658-D		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1050	OR10G1P	H38g90 0			AE000658-C			FL
1051	OR10G2	H38g90 1			AE000658-B		yes	FL
1052	OR5Tn	H38g90 2					yes	FL
1053	OR7EnP	H38g90 3						FL
1054	OR7EnP	H38g90 4						FL
1055	OR4AnP	H38g90 5						FL
1056	OR4C1	H38g90 6			HSHTPCRX11	+		FL
1057	OR1EnP	H38g90 7						
1058	OR7KnP	H38g90 8						FL
1059	OR4CnP	H38g90 9						FL
1060	OR1RnP	H38g91 0						FL
1061	OR5AUn	H38g91 1					yes	FL
1062	OR4Cn	H38g91 2					yes	FL
1063	OR4Cn	H38g91 3					yes	FL
1064	OR13DnP	H38g91 4						FL
1065	OR5n	H38g91 5	DSU116			+		
1066	OR2Hn	H38g91 6	DSU150			+		
1067	ORn	H38g91 7	DSU151			+	put	
1068	ORn	H38g91 8	DSU17			+		
1069	ORn	H38g91 9	DSU18			+		

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1070	ORn	H38g92 0	DSU35			+		
1071	OR6Fn	H38g92 1	DSU41			+		
1072	ORn	H38g92 2	DSU49			+		
1073	ORn	H38g92 3	DSU50			+		
1074	OR10An	H38g92 4	DSU57			+		
1075	ORn	H38g92 5	DSU58			+		
1076	OR2Ln	H38g92 6	DSU59			+		
1077	OR10Jn	H38g92 7	DSU60			+		
1078	OR1Kn	H38g92 8	DSU63			+		
1079	OR10Dn	H38g92 9	DSU7			+		
1080	ORn	H38g93 0	DSU32			+		
1081	OR2Ln	H38g93 1	DSU38			+		
1082	ORn	H38g93 2	DSU62			+		
1083	ORn	H38g93 3	DSU48			+		
1084	OR2n	H38g93 4	DSU111			+		

Table 2

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SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
153	OR10D3	0	11	137.96SDVISV	69	M	AC074177.4	12106 ... 13038
154	OR7EnP	4	4	11.58	MVACGVLDLHIIDSFAL	53	R	AF091580.1	7 ... 663
155	OR1D5	0	17	3.75	LVVTNLLYLLLLTGIFT	49	M	AF073967.1	2 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
156	OR10Nn P	4	11	138.02	LQSGGVVHILFGNVLAT	82	M	AC074177.4	159287 ... 158526
157	OR2F1	0	7	148.62	LLGGFTSSVQIISSLLT	56	M	AF073974.1	41 ... 649
158	OR7EnP	7	4	11.58	MAGGELLDLHILPALGL	54	M	AF073989.1	547 ... 1515
159	OR8FnP	6	11	137.96	LLVICEMGAHCVC SNIF	75	M	AC069561.1 0	51687 ... 50743
160	OR2Q1P	2	7	148.62	LLCGFSANMEIVSGVIL	49	M	AC020865.3	190954 ... 189954
161	OR2W1	0	6	33.74	LMGSCMINVLLVLGIVT	88	M	AF102516.1	52 ... 669
162	OR7EnP	7	4	11.58	MVACGVLDLHITHSFGL	53	R	AF091580.1	7 ... 663
163	OR6B1	0	7	148.62	LIMCCGIIAKFDLAIFF	61	M	NM_010983. 1	178 ... 975
164	OR10Kn	0	1	154.34	MLGSSACVVTILGALI	79	M	AC073778.1	168744 ... 167803
165	ORnP	13	11	138.02	VPYCIGGHLICLSLSS	33	M	AC074177.4	12106 ... 13038
166	OR4F2P	4	6	186.49	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
167	OR7EnP	3	4	11.58	MVACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
168	OR1F2P	0	16	6.15	MSADNGVNLHLIEAVTT	72	R	M64377.1	1 ... 939
169	OR2P1P	7	6	33.74	FGGSCMSNQSALVRXSV	48	M	NM_008762. 1	1 ... 936
170	OR7E43 P	5	4	5.57	MAGGELFDLHIMPAFGL	54	M	AF102536.1	22 ... 669
171	OR4F1	4	6	0.23	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
172	OR7E55 P	5	3	89.94	MAGDEFDLHILPAFGL	53	M	AF073989.1	547 ... 1515
173	OR13Dn	0	9	86.89	MLGSCWITLQLMTNSLI	61	M	AC023789.5	371264 ... 372220
174	OR4CnP	3	16		AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
175	OR10D1 P	1	11	137.96	LHGCCGFQFLGSMPS	83	M	AC074177.4	128803 ... 129726
176	OR4Cn	0	16		LHGGIVGHVQLVNSICL	86	M	AB030895.1	1 ... 924

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
177	OR8GnP	0	11	137.96	LSAICGLGIHFVLSNIM	73	M	AC074177.4	106297 ... 105361
178	OR13CnP	2	9	86.85	MFGACGGNLQLMASFLG	82	M	AJ251154.1	2703 ... 1747
179	OR4CnP	5	16		LHEAIVLHIQFINSCL	61	M	AF102522.1	40 ... 660
180	OR13CnP	0	9	86.81	MLGTCGINVQFMATFIT	69	M	AJ133425.1	61 ... 1014
181	OR4CnP	0	16		LHGGIMGHIQLVNSMCL	63	M	AB030895.1	1 ... 924
182	OR51BnP	0	11		AHSVSGRSPVRPLITIL	76	M	AF071080.2	15931 ... 16851
183	OR7E5P	2	11	51.76	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
184	OR13CnP	0	9	86.77	MFGSCVSNVQLMSNFLL	71	M	AJ251154.1	2703 ... 1747
185	OR4Sn	0	16		LHGGIAAHLQLVNSISA	56	M	AB030895.1	1 ... 924
186	OR51BnP	4	11		VHYPEWRSPPPPLVIFL	72	M	AF071080.2	15931 ... 16851
187	OR6JnP	1	14	2.72	CFGTFFGSFPLDLVIC	50	R	M64378.1	1 ... 933
188	OR51BnP	0	11		SHAISGRSPISPQTTVL	76	M	AF071080.2	26330 ... 27262
189	OR7EnP	2	11	71.8	MFACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
190	OR2An	0	6	144.32	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
191	OR7E22P	3	3	89.94	MVACDVLDLHIIDSFGL	56	M	AF073989.1	547 ... 1515
192	OR7E4P	2	11	71.8	IVACDVLDLHIMHSFGL	55	M	AF102536.1	22 ... 669
193	OR7E66P	9	3	89.94	MAGGELLEFLHIMPAFGL	55	M	AF073989.1	547 ... 1515
194	OR6Mn	0	11	138.18	TFGTFGGSFVNLSVIS	50	M	NM_010991.1	1 ... 939
195	OR2ALnP	11	11	112.69	ILGTCASNFDFFNHL	32	M	AL359352.1	85325 ... 86251
196	OR6MnP	2	11	138.18	TGGTFGGSCPVNLSILT	50	M	NM_010991.1	1 ... 939
197	OR4D1	0	17	60.7	IHGGVAGHVQLMNSLVI	90	M	AC019272.4	62255 ... 61317
198	OR5D2P	3	11	51.09	LCVVTTWCTLFTSANES	48	M	AC073947.3	29192 ... 30115

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
199	OR7E38P	7	7	95.91	MAGGELFHLHIMPAFGL	55	R	AF091580.1	7 ... 663
200	OR4D2	0	17	60.7	IHGGVAGHVQLKNSLDV	89	M	AC019272.4	183633 ... 182701
201	OR7E7P	4	7	95.91	MIACGVLDLHIIDSFGL	56	R	AF091580.1	7 ... 663
202	OR5AHnP	0	19	68.97RSGIMC	77	M	AC020957.2	48184 ... 49107
203	OR2U2P	5	6	33.53	LVYSCIVNIPYTMCIIVV	49	M	AC044846.2	105668 ... 104736
204	OR2U1P	2	6	33.53	LVCTCMINILCCVVIFA	54	M	AF102516.1	52 ... 669
205	OR2H2	0	6	33.19	ILGTCVIEVQSVASILV	89	M	AL078630.1	41097 ... 40165
206	OR2H5P	7	6	33.19	FLGTCVIEVQSMASILV	84	M	AL078630.1	41097 ... 40165
207	OR2In	0	6	33.19	LLGSCASNAQLMARILL	74	M	AL078630.1	151152 ... 150391
208	OR11HnP	5	13		IFNTCLCWIPLCLSVIG	60	M	AF121972.1	171 ... 1109
209	OR7EnP	6			AAACDVIDLHITHSFGL	56	M	AF073964.1	41 ... 649
210	OR9In	0	11	54.06	FTAGCGCGLRCIFGVIA	50	R	AF091579.1	7 ... 663
211	OR2AFnP	11	X	140.17	MLGTGCHVTLAGISTLL	43	R	L34074.1	73 ... 1011
212	OR13KnP	5	X	140.17	MFGMCVIIHILGIGTLL	43	R	L34074.1	73 ... 1011
213	OR13Cn	0	9	86.77	MFGSCVSNVQLLSNFL	68	M	AJ251154.1	2703 ... 1747
214	OR13Fn	0	9	86.77	MLGSCGTTVESMISLLM	55	M	AJ133428.1	61 ... 1017
215	OR9Qn	0	11	54.08	FTGSCGASVRSIFAVIA	47	M	AF146372.1	509 ... 1456
216	OR2TnP	1	1	254.77	ILIGFGGDMVMCCMLI	71	M	AF102527.1	22 ... 669
217	OR4Kn	0	14	0.08	IHVGMIVHSHFTNSISS	56	M	AF259072.1	104176 ... 105099
218	OR2B8P	0	6	31.6	LLGSCTINLQLLVSVILV	62	R	L34074.1	73 ... 1011

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
219	OR2Tn	0	1	254.77	MLAGVALDLLITCCMLT	57	M	AF102527.1	22 ... 669
220	OR4Kn	0	14	0.08	IHTGIAMHSQFMTSIAS	53	M	AF259072.1	104176 ... 105099
221	OR2A4	0	6	144.76	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
222	OR7EnP	6	2	161.53	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
223	OR4Kn	0	14	0.08	MHGGILVHSQFMTSIAV	57	M	AF259072.1	104176 ... 105099
224	OR13In P	6	9	86.85	MYGSCVLNNVIGKTLL	41	M	AJ251155.1	15491 ... 16423
225	OR7EnP	8	2	161.53	MVACDVLDLHIFDFGL	54	M	AF073989.1	547 ... 1515
226	OR6Jn	0	14	2.72	CFGTFFGSFPLDLVIC	50	R	M64378.1	1 ... 933
227	OR4Mn	0	14	0.08	LHGAMLGHIQLMSSISV	54	M	AC019272.4	183633 ... 182701
228	OR4VnP	10	11	51.09	IHGIIVLHFQMVNSFAV	50	M	AB030896.1	1 ... 906
229	OR6Xn	0	11	138.36	AFGTFSVICQLGATVIG	46	M	AF106007.1	178 ... 975
230	OR51Gn	0	11	3.7	LHSSSSRLPLLGVVTVV	55	M	NM_013617.1	1 ... 921
231	OR6EnP	3	14	2.72	SFGTFCTLIPLGIASLG	82	M	NM_010991.1	1 ... 939
232	OR4NnP	2	14	0.08	LHGGGAGHIQLMNSMTL	54	M	AC019272.4	62255 ... 61317
233	OR6MnP	7	11	138.18	IFGTFGGARLVXSMTV	37	R	M64378.1	1 ... 933
234	OR4Nn	0	14	0.08	LHGGGAGHIQLMNSMTL	57	M	AC019272.4	62255 ... 61317
235	OR4Cn	0	11	51.09	LHGGIGGHIQFVNSMCA	65	M	AF102522.1	40 ... 660
236	OR4KnP	4	14	0.08	IHAGMGTHSQFMDSMGT	51	M	AF259072.1	104176 ... 105099
237	ORnP	8	11	137.59	AIAITVVVAHAAAGVVA	35	M	AC069559.8	73704 ... 74636
238	OR5D3	0	11	51.15	FCVVTAWCTYFISANES	46	R	U50948.1	34 ... 978
239	OR2G1P	6	6	33.53	LLGSCVSNIQVLASLLL	84	M	AL359352.1	85325 ... 86251

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
240	OR4Kn	0	14	0.08	IHTGMIVHSQFINSLS	51	M	AF259072.1	104176 ... 105099
241	OR8BnP	2	11	137.59	LCVFSGMGAHNVIVGIV	68	M	AC069559.8	120212 ... 119283
242	OR2B2	0	6	31.47	LLGSCASNQWLISFLI	89	R	L34074.1	73 ... 1011
243	OR7EnP	3	2	73.87	MVACDVLDLRIIDSFGL	54	M	AF073989.1	547 ... 1515
244	OR4KnP	3	14	0.08	IHTGIVVHSQFMTSIAI	57	M	AB030896.1	1 ... 906
245	OR2AD1 P	6	6	33.87	FLGACTSSIVLVFGFLV	51	M	AL136158.1 4	162423 ... 161461
246	OR1AA nP	8	X	140.17	MIVDNTIVLHLIIGVII	48	M	AC068902.1 1	144125 ... 143193
247	OR1E3P	1	17	2.99	MLGVSLHLHLMMGILI	74	R	M64392.1	1 ... 942
248	OR8BnP	3	11	137.59	FCVFSGMGAHNIVVGIV	63	M	AC069561.1 0	96653 ... 95690
249	OR5Hn	0	3	104.18	FAGTCFGHIHLVLSIQF	55	R	AF091575.1	52 ... 663
250	OR1G1	0	17	2.99	LMVMAAMHLHLITGTGI	56	R	M64392.1	1 ... 942
251	OR5HnP	2	3	104.18	FAVTCGGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
252	ORnP	5	X	140.17	MLVTCSHHFLSFTGIWS	36	R	U50948.1	34 ... 978
253	ORnP	11	X	140.17	LIVTFAKITTTQDHHHH	29	M	AC069561.1 0	127636 ... 126698
254	OR4PnP	2	11	51.09	LHGDIAGHSQVNSISL	51	M	AB030895.1	1 ... 924
255	OR13Hn	0	X	140.17	TLATCTTVAMLITSTLL	47	M	AJ251154.1	35662 ... 36615
256	OR7D1P	5	19	11.38	VMAGTAIFVHLLATLGF	64	R	AF091580.1	7 ... 663
257	OR4KnP	2	18	47.77	IHNIGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
258	OR7E24	1	19	11.38	MVACDLIDLHIIMGFGL	60	R	AF091580.1	7 ... 663
259	OR51N nP	2	11	3.6	LHGFSARSPSLGVLTV	49	R	AF079864.1	632 ... 1576
260	OR7E18 P	6	19	11.38	VAGCDLLDLHIMLAFGL	59	M	AF102536.1	22 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
261	OR7E19P	2	19	11.38	MYVCDVLNLHIMDSFGL	58	M	AF073989.1	547 ... 1515
262	OR7E41P	7	11	14.36	IVVCDMLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
263	OR2R1	3	7	148.69	LLGGFVVNMELISSVLV	77	M	AF073974.1	41 ... 649
264	OR10ACnP	7	7	148.69	MVGGCGRVGLLLACLLL	46	M	AC073778.1	168744 ... 167803
265	OR51Ln	0	11	3.79	LHTFSARVPTLGVVTLV	54	R	AF079864.1	632 ... 1576
266	OR52JnP	3	11	3.79	MHTGSSRLPILGVALDA	57	M	AF121979.1	53 ... 1106
267	OR9LnP	9	8	45.22	TVVNNFFFFFFFIFDLIA	37	M	AC069561.1 0	147203 ... 146274
268	OR51PnP	4	11	3.79	MHSISARLPALGVVSM	48	M	AF071080.2	2641 ... 1697
269	OR5HnP	4	3	104.18	FAVTCLGHIHFFFSIQL	50	R	AF091575.1	52 ... 663
270	OR51An	0	11	3.79	EHSVSVKLPFTYFGCLV	48	R	AF079864.1	632 ... 1576
271	OR5HnP	6	3	104.18	FAVTCLGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
272	ORnP	11	17	17.43	LLPCILSIIALYYYYYY	27	M	AL359352.1	9138 ... 8177
273	OR52En	0	11	3.79	MHTGSARFPFFYCAILF	57	M	AF121979.1	53 ... 1106
274	OR5Hn	0	3	104.18	FVVTCLGHIHFVFAVQF	53	R	AF091575.1	52 ... 663
275	OR4CnP	3	11	50.21	VHRGVVGHIQFVNSICL	73	M	AF102522.1	40 ... 660
276	OR52En	0	11	3.79	MHTLSGRFPSLYCANLF	60	M	AF121979.1	53 ... 1106
277	OR10Dn	0	11	138	LHGCCGIHILLGNVLSI	86	M	AC074177.4	12106 ... 13038
278	OR5HnP	2	3	104.18	FVVTCLGHIHFVFAIQF	54	R	AF091575.1	52 ... 663
279	OR13An	0	10	47.91	LTASLALNIHLIADYGV	67	M	AF102520.1	16 ... 669
280	OR5HnP	2	3	104.18	FGGTCLGHIHILLSIQF	57	R	AF091575.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
281	OR5Kn	0	3	104.47	FCETCGAHIHLFSVQF	45	M	AC069559.8	36251 ... 35322
282	OR7EnP	9	21	17.99	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
283	OR4DnP	6	8	77.48	IHGGVAGHVQVMNSLVI	87	M	AC019272.4	62255 ... 61317
284	OR2ARn P	0	3	30.89	MLGSC.....	71	M	AJ251154.1	56533 ... 57369
285	OR7E29 P	4	3	136.03	MAGGELLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
286	OR4CnP	3	11	51.12	AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
287	OR5PnP	2	11	6.93	LVGTCVGNTFCPSSIIV	74	M	AF121977.1	262 ... 1197
288	OR7EnP	5	3	136.04	MVACGVLDLHIIGSFGL	52	R	AF091580.1	7 ... 663
289	OR56An	0	11	4.73	MNLPSFRLPILQAGLLS	41	M	AF121975.1	50 ... 1012
290	OR56An P	9	11	4.73	KNQAFFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
291	OR5Pn	0	11	6.89	LAATCVAISYSLSSIIV	63	M	AF121977.1	262 ... 1197
292	OR7E53 P	5	3	136.04	MAGGEFPDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
293	OR5Pn	0	11	6.89	LVGTCMGNTFCPSSIIA	83	M	AF121977.1	262 ... 1197
294	OR52Ln	0	11	4.73	MHSSSVRLPFLGMAVIL	59	M	AF121976.2	474 ... 1307
295	OR5E1	3	11	6.89	LGATXGYNIQLLFSNLG	51	R	U50948.1	34 ... 978
296	OR56An P	3	11	4.73	MNLASFRMAILPPPPPP	39	M	AF121976.2	474 ... 1307
297	OR4KnP	2	8	88.25	IHTGMIVHSQFIDS...	57	M	AB030896.1	1 ... 906
298	OR52Ln	0	11	4.73	MHSSSVRLPFLGVAVVL	59	M	AF121976.2	474 ... 1307
299	OR7EnP	1	4	74.82	MVF.....	55	R	AF091580.1	7 ... 663
300	OR52Xn P	5	11	4.73	MHSASLXLSFLAVALGG	51	M	AF121976.2	474 ... 1307
301	ORnP	13	4	74.82	STGCKGRKXLKLVRFQ	24	R	M64386.1	130 ... 975
302	OR56An	0	11	4.73	MNLTSFRVPVLQAGLLS	84	M	AF121981.1	89 ... 475

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
303	OR56An P	10	11	4.73	LI...GMMXNL...KKK	60	M	AF121981.1	89 ... 475
304	OR1R1P	5	17	3	MVGISAVHLHLIEGVVA	48	M	AF073967.1	2 ... 649
305	OR52En P	2	11	3.79	MHTGSGRSPFLYGAILF	64	M	AF121979.1	53 ... 1106
306	OR51An P	4	11	3.7	EHTVALKLPLLGA GSTL	46	R	AF079864.1	632 ... 1576
307	OR51An	0	11	3.7	EHSVSVKLPFTYFGCLV	48	R	AF079864.1	632 ... 1576
308	OR4CnP	1	11	51.12	VHGGVVGHVQFVNSICL	75	M	AF102522.1	40 ... 660
309	OR52Jn P	9	11	3.79	MHTGACRFPI LGVVYLN	58	M	AF121979.1	53 ... 1106
310	OR4RnP	9	11	51.12GGGVXSVNGNYL	66	M	AF102522.1	40 ... 660
311	OR52Jn	0	11	3.79	MHTGACRLPMLGVVFN	58	M	AF121976.2	474 ... 1307
312	OR4CnP	3	11	51.12	VHGGGVGHIQFINSICL	76	M	AF102522.1	40 ... 660
313	OR51An P	2	11	3.79	EHSASAKLPFTYFVTGL	83	M	AF121985.1	2 ... 478
314	OR7EnP	15	12	93.55	IVVCDLLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
315	OR5MnP	2	11	52.17	CIVLHVYLMERMVASNQ	54	M	AF102528.1	52 ... 669
316	OR10AB nP	1	11	6.93	MLASCAVFCITILSVLG	47	M	AC073778.1	168744 ... 167803
317	OR52Sn P	2	11	3.79	MHSTSARLPHLSVATGV	54	M	AF121976.2	474 ... 1307
318	OR5Mn	0	11	52.14	CIVHIFYTAAWMLANFY	49	R	AF091579.1	7 ... 663
319	OR10Sn	0	11	138.1	LHASCIIHIHLMSIVAG	61	M	AF259072.1	32953 ... 32000
320	OR5MnP	4	11	52.14	CIVHIFYTTAWMLANFY	48	R	AF091579.1	7 ... 663
321	OR10Gn	0	11	138.1	LHGSCGSHVQLIDIVAG	61	M	AF259072.1	55611 ... 54658
322	ORnP	20	11	29.15	ILGIYEGSAHYFIILFL	33	M	AL365337.1	192661 ... 191711
323	OR5MnP	2	11	52.19	CIVYIGYSMEWMVANLS	54	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
324	OR10Gn P	10	11	138.1	LYGSCWGHLPYIVIKFT	30	M	L14567.1	17 ... 667
325	OR10Tn P	1	1	154.34	LVACCACTIVLILSVLV	57	M	X92969.1	8035 ... 8961
326	ORnP	16	11	52.17	LAAPLLLVLVLAASAAA	33	R	M64376.1	1 ... 999
327	OR10Rn P	11	1	154.5	MLAVFTICVFLIGGALV	47	M	AC023611.2	108224 ... 107271
328	OR5MnP	2	11	52.16	CIVHLVYTMEWMVANFY	49	R	AF091579.1	7 ... 663
329	OR7EnP	4	8	6.68	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
330	OR10Tn	0	1	154.27	LLACCLTIVALLSVIV	58	M	AC012302.5	54283 ... 55224
331	OR1E1	0	17	3.04	MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
332	OR5BKn P	4	12	42.11	STGGAIAIMDFLSQWGL	46	M	AF073965.1	2 ... 643
333	OR5MnP	3	11	52.17	CIVHIVYTMEWMVANLF	48	R	AF091579.1	7 ... 663
334	OR3A3	0	17	3.06	LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
335	OR10AD nP	1	12	42.11	TFGVCTFNFLIIDAVIS	44	M	AF247657.1	1 ... 945
336	OR10Rn	0	1	154.5	MLAICAGATVLCIGVLV	56	M	AC073778.1	168744 ... 167803
337	OR5TnP	4	11	51.94	MCGTCAAHIAFFVIEV	51	M	AF121977.1	262 ... 1197
338	OR4GnP	15	7	0.23	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
339	OR6Yn	0	1	154.5	LVVCYGCTIKFDLAVII	61	M	NM_010983. 1	178 ... 975
340	OR1E2	0	17	3.15	MLSDSLHLHLIMGILI	80	R	Y07557.1	1 ... 942
341	OR8Hn	0	11	51.94	MVGACGINVNWILATLV	51	M	NM_013728. 1	1 ... 948
342	OR4Fn	0	7	0.23	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
343	OR10Kn	0	1	154.27	MLGCSACVIILICVLI	83	M	AC073778.1	168744 ... 167803
344	OR7LnP	11	X	140.17	MLGVCGHGTNLXFFFFI	32	M	AL133160.1	63932 ... 64759
345	OR8InP	7	11	51.94	MVVCCMINVSVSLATLG	44	R	M64386.1	130 ... 975

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
346	OR10Rn P	0	1	154.5	MLAVCTSI VGFIFGV LV	54	M	AC073778.1	168744 ... 167803
347	OR2AFn P	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
348	OR8Kn	0	11	51.94	LEIILVYVFLKIFSNLF	55	M	AF102528.1	52 ... 669
349	ORnP	7	10	127.57	S.CCCLLTYYIIHHHHHH	31	M	AC020958.1	164590 ... 163746
350	OR8KnP	10	11	51.94	MIIILYQMVKIFSNLF	35	M	AC073945.4	152209 ... 153150
351	OR51Hn	0	11	3.6	MHGISSRVPVLGVVTL	49	R	AF079864.1	632 ... 1576
352	OR7EnP	5	3	136.03	MVACGVLDLHIIDSFGL	51	M	AF073989.1	547 ... 1515
353	ORnP	8	3	56.17	LLLLFLIIEQH.....I	32	R	M64376.1	1 ... 999
354	OR5BMn P	20	3	103.93	KXNKCTLSSSLMVFIQF	30	M	AF146372.1	509 ... 1456
355	OR10Gn P	0	11	138.1	LHGCGGSHFQFTDILAT	63	M	AF259072.1	55611 ... 54658
356	OR2Yn	0	5	209.23	LLGSCAANIQLMARVVV	74	M	AC044846.2	139468 ... 138536
357	OR10Dn P	1	11	138.1	LHGCGGSHVLLSNVVM	66	M	AC074177.4	128803 ... 129726
358	OR3BnP	7	X	158.48	IHAPSILNTYLLSFVAA	37	M	AL136158.1 4	29455 ... 30402
359	OR8Dn	0	11	138.1	LCVICAVDIHCIGNMA	62	R	X80671.1	203 ... 1129
360	OR5RnP	0	11	52.13	LLMICVYVFHIFADMS	68	M	AF102528.1	52 ... 669
361	OR10Gn	0	11	138.1	LHGSCGSHVQLINIVAG	58	M	AF259072.1	55611 ... 54658
362	OR5BDn P	12	11	53.74	MTGTCVVIHRALSSITP	39	M	NM_013728. 1	1 ... 948
363	OR5ALn P	1	11	52.13	VIVVLSYVVQALIANTC	52	M	AC073947.3	29192 ... 30115
364	OR52Hn P	3	11	4.15	LHFVSGRPCLGVPTVT	59	M	AF121975.1	50 ... 1012
365	OR10Gn	0	11	138.1	LHGGCSSHVQLITVVAG	56	M	AF259072.1	55611 ... 54658

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
366	OR5Mn	0	11	52.17	CIVHIVYTMEWMVANLF	52	M	AF146372.1	509 ... 1456
367	OR51Mn	0	11	4.15	MHSFSIRAPILGVVTVL	50	M	NM_013617.1	1 ... 921
368	OR6Tn	0	11	138.1	SFGTFAAWCPLALSVLG	52	M	NM_010991.1	1 ... 939
369	OR6DnP	5	10		SLGSFVVLGLKALVVLT	69	R	AF034903.1	85 ... 1053
370	OR4B1	0	11	45.36	IHGVIGGHIQVVSFSF	62	M	AF102522.1	40 ... 660
371	OR5ALnP	4	11	52.13	VISVGYMIQALIANVC	50	M	AF146372.1	509 ... 1456
372	OR51Qn	0	11	4.15	FHSFSACAPSLGLAIIV	49	M	NM_013617.1	1 ... 921
373	OR4Dn	0	11	138.1	LHGGIAGHVQLMNNVTM	63	M	AC019272.4	62255 ... 61317
374	OR52Nn	0	11	4.58	MHTGSLRLPSLGVAIGF	52	M	NM_013619.1	118 ... 969
375	OR4Xn	0	11	45.36	MHGGGAIGHGQLINGISV	58	M	AB030896.1	1 ... 906
376	OR8Jn	0	11	52.03	LLIVVLYTVVYVSANVG	77	M	X89682.1	2 ... 472
377	OR51JnP	2	11	4.15	MHSMsIKLPLLGIIVTFL	46	M	AF071080.2	15931 ... 16851
378	OR10Gn	0	11	138.1	LHGSCSSHVQLIDIVAG	60	M	AF259072.1	55611 ... 54658
379	OR52En	0	11	4.58	MHTGTVRLPFLGVIIID	66	M	AF121979.1	53 ... 1106
380	OR4Xn	0	11	45.36	LHGGIIGHAQLINGLSI	64	M	AB030895.1	1 ... 924
381	OR10A2	1	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
382	OR5Mn	0	11	52.14	CIVHVYVICWMIANFY	49	R	AF091579.1	7 ... 663
383	OR52En	0	11	4.58	MHTGSVRFPFLISVVGI	59	M	AF121979.1	53 ... 1106
384	OR8Kn	0	11	51.94	LLIGLIYILVKIFADLS	53	M	AF146372.1	509 ... 1456
385	OR10An	0	11	5.66	MFGACASVVQWAATFIF	89	M	AF247657.1	1 ... 945
386	OR8LnP	3	11	52.13	LIVVMSYVLQLLANTF	51	M	AF102528.1	52 ... 669
387	OR5BPnP	8	11	52.82	VVVVVGGSIVPPVGLHL	43	R	U50948.1	34 ... 978
388	OR52Nn	0	11	4.58	MHTGSARLPFLGVAIGF	54	M	AF121976.2	474 ... 1307

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
389	ORnP	7	11	45.36	WWWIALLR.AAAAAK	28	M	X89686.1	32 ... 472
390	OR8JnP	1	11	51.94	LLIVILQTTVCVFSNLF	99	M	X89682.1	2 ... 472
391	OR5Mn	0	11	52.24	CIVIFVYNSQLMVATLS	50	R	AF091579.1	7 ... 663
392	OR52En	0	11	4.58	MHTVSIRMPLLGSILL	66	M	AF121979.1	53 ... 1106
393	OR5Tn	0	11	51.94	VCGTCAAHIHALFVIEV	52	M	AF146372.1	509 ... 1456
394	OR52NnP	5	11	4.58	MHTGSVQLPFLGAAIGF	51	M	NM_013619.1	118 ... 969
395	OR4B2P	6	11	45.36	IFGIIGRHVQVNSELS	53	M	AB030896.1	1 ... 906
396	OR51KnP	6	11	4.15	MHSCSGKLPLLGIVNFL	51	M	NM_013617.1	1 ... 921
397	OR52QnP	10	11	4.58	MYTGSVRFPFLFVAVGI	45	M	AF121979.1	53 ... 1106
398	OR4Fn	0	15	86.21	IHGGMIIHIQFVNSISA	50	M	AF102522.1	40 ... 660
399	OR11MnP	1	12	41.92	FSAACGSFTL.....	48	M	AL359381.1	175785 ... 176720
400	OR52NnP	0	11	4.44	MHTGSARLPFLGVAIGF	57	M	NM_013619.1	118 ... 969
401	OR56An	0	11	4.58	MNLASFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
402	OR5AwnP	14	X		LXADFTSNLPTTSSNVV	39	R	X80671.1	203 ... 1129
403	OR52NnP	0	11	4.51	MHTGSARLPFLGVAIGF	55	M	AF121976.2	474 ... 1307
404	ORnP	15	X		ISCIFELTLPLPSNVV	31	M	AC073947.3	29192 ... 30115
405	OR52EnP	6	11	4.58	VHSVSVRMPILGNIILL	62	M	AF121979.1	53 ... 1106
406	OR5BHnP	9	X		MVASCGGKTVSLCGTLT	40	M	NM_013728.1	1 ... 948
407	OR4QnP	1	15	1.66	IHGAMAGHMQLMNSLSV	60	M	AC019272.4	62255 ... 61317
408	OR51En	0	11	3.04	MHSGSARLPFLGVIAIL	60	R	AF079864.1	632 ... 1576
409	OR11KnP	2	15	1.66	FSGYGFCITLLITFVFI	53	M	AF121972.1	171 ... 1109
410	OR12D1P	1	6	33.02	LHGSATIHLMSTGIAG	76	M	AL133159.4	16108 ... 15185

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
411	OR4NnP	3	15	1.61	LHGGGAGHIQLMNSMTM	55	M	AC019272.4	62255 ... 61317
412	OR11A1	0	6	33.02	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
413	OR10C1	0	6	33.02	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
414	OR2H1	0	6	33.02	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
415	OR9RnP	8	12	59.71	LAVGGGCNIQFLLSITT	54	R	AF091579.1	7 ... 663
416	OR4FnP	0	7	0.53VLHFQFVNSICG	50	M	AB030896.1	1 ... 906
417	OR7D4	3	19	11.31	VMAGTAIFVHLLATLGF	67	R	AF091580.1	7 ... 663
418	OR7E25 P	3	19	11.31	MIACSVLDLHIVIGFGL	61	R	AF091580.1	7 ... 663
419	OR2D2	0	11	5.69	LLGCCGSVVDFITGILI	65	M	AF073987.1	2 ... 649
420	OR10An	0	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
421	OR2WnP	3	1	254.49	LLGGCVCQGHVVLAVVS	54	R	L34074.1	73 ... 1011
422	OR7E16 P	8	19	11.31	IAGCDLLDLHIMLALGL	60	M	AF102536.1	22 ... 669
423	OR52Pn	0	11	4.44	MHCMSARLPCLGAAVIV	59	M	AF121976.2	474 ... 1307
424	OR6AnP	4	11	5.66	LLGCCGGIVKLDLAILG	94	R	M64386.1	130 ... 975
425	OR7D2	0	19	11.24	VMPITVITLHLIMTLGF	61	R	AF091580.1	7 ... 663
426	OR52Un P	3	11	4.44	LHSASVRFPMLGVAVAY	52	M	AF121976.2	474 ... 1307
427	OR2AGn	0	11	5.6	MLGGDTLSIYYVMGFLP	55	M	AF102527.1	22 ... 669
428	OR7G3	0	19	11.24	ILVGNLVDLHMVVTLG	64	R	AF091580.1	7 ... 663
429	OR56Bn P	3	11	4.44	IHVGSFRFPVLQLAGMS	41	M	AF133300.1	25713 ... 26573
430	OR2AGn P	1	11	5.51	MLGSDTLIGHYITGFL	55	M	AF102527.1	22 ... 669
431	OR56Bn	0	11	4.44	MHVASFRCVQLALMS	39	M	NM_013619. 1	118 ... 969
432	OR6AnP	5	11	5.51	LLGCCGGIVKLDLAILG	93	R	M64386.1	130 ... 975
433	OR4FnP	4	19	63.23	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
434	OR6Wn	0	7	148.04	SFGSFAVSSPQDLSFVT	47	M	NM_010991. 1	1 ... 939
435	OR4Mn	0	15	1.59	LHGAMLGHIQLMSSISV	52	M	AF259072.1	104176 ... 105099
436	OR52Yn P	13	11	3.6	VVVVVVLQWPVMGMAVDF	29	M	AF133300.1	46551 ... 47498
437	OR11Hn P	2	15	1.78	FFGTCLCWIPLCLSVIG	61	M	AF121972.1	171 ... 1109
438	OR9An	0	7	148.04	LSGTFFVFSWPALMAILG	46	M	NM_010991. 1	1 ... 939
439	OR5Mn	0	11	52.19	CILLFFYDFQLMSANLS	50	M	AC069563.9	129775 ... 130725
440	OR6Vn	0	7	148.04	FFGSFAAAPTSDMAFVS	45	M	NM_010991. 1	1 ... 939
441	OR4Nn	0	15	1.61	LHGGGAGHIQLMNSMTL	53	M	AC019272.4	62255 ... 61317
442	OR51An P	4	11	3.6	EHTDSLILPFTGLACMS	43	M	NM_013617. 1	1 ... 921
443	OR9PnP	10	7	148.04	FGSNSFEHLVFIHSLLM	39	M	NM_010983. 1	178 ... 975
444	OR4H6P	3	15	1.66	MHGCI LGHVQLVNSISG	59	M	AF259072.1	104176 ... 105099
445	OR51Fn P	2	11	3.6	MHTFSLRLPLLGLTTI	48	R	AF079864.1	632 ... 1576
446	OR7E1P	3	11	68.1	MVACGVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
447	OR51Tn	0	11	3.6	MHSLSVRFPLAGLQNT	44	R	AF079864.1	632 ... 1576
448	OR2Vn	0	13	104.15	IVVGGSFDIQVICMLF	84	M	AF102535.1	16 ... 669
449	OR51Hn P	7	11	3.6	MHGG SARAPVLGAVIIL	51	R	AF079864.1	632 ... 1576
450	OR51An	0	11	3.6	EHTVSIRLPFTGIAC TL	48	M	AF071080.2	26330 ... 27262
451	OR2AIn P	2	5	209.13	YLGSCLSNFHLMARILL	55	M	AC044846.2	112743 ... 113748
452	OR2F2	0	7	148.74	LLGGFTSNVQIISSLLT	54	M	AF073974.1	41 ... 649
453	OR1F12	0	6	31.61	MMANNAINLHMVTVIFV	58	M	AC023167.7	60743 ... 61663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
454	OR7G1P	0	19	11.24	ILAGSLMDVQMIASFGI	60	R	AF091580.1	7 ... 663
455	OR7G2	0	19	11.24	ILAGNLTNLLMIAAFGV	61	R	AF091580.1	7 ... 663
456	OR1M1	0	19	11.24	MHGISAFITHLIVAVIT	89	M	X89689.1	32 ... 472
457	OR51UnP	1	11	2.89	VTDDN.....	48	R	AF079864.1	632 ... 1576
458	OR52Hn	0	11	4.19	MHFVSGRIPDLGVPTVS	59	M	AF121975.1	50 ... 1012
459	OR1F1	0	16	6.15	MFVDNGVNLHLIEGVMT	75	R	M64377.1	1 ... 939
460	OR10PnP	0	16	87.09	MIGICTTTTHLVATFII	48	M	AF247657.1	1 ... 945
461	OR4FnP	4	19	7.9	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906
462	OR2T1	0	1	254.77	HLVGFGGDLIMCCMLI	92	M	AF102527.1	22 ... 669
463	OR7EnP	9	19	22.8	VAGCDLLDLHIMLAFGL	60	M	AF102536.1	22 ... 669
464	OR51Gn	0	11	3.6	LHSFSVRLPLMGVITVI	57	M	NM_013617.1	1 ... 921
465	OR2Tn	0	1	254.77	MVAGFGLDTFIMCCMLI	67	M	AF102527.1	22 ... 669
466	OR5BGnP	2	11	51.27	AAAAAGGSIHNLFAVEI	52	R	U50948.1	34 ... 978
467	OR5WnP	3	11	51.27	MGADCLVDIHCMFVVAC	51	M	AF146372.1	509 ... 1456
468	OR51Sn	0	11	3.6	MHSVSARLPLLLVLMGD	42	M	AF071080.2	26330 ... 27262
469	OR5WnP	1	11	51.27LVFIES	55	M	AC074177.4	107189 ... 107708
470	OR51AnP	3	11	3.6	EHTDSLILLPTGVAMMD	46	M	NM_013617.1	1 ... 921
471	OR5Dn	0	11	51.21	FCGVTCWCILFCIANES	46	M	AF146372.1	509 ... 1456
472	OR7EnP	4	4	5.55	MVACGVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
473	OR51Fn	0	11	3.6	MHTFSSRPVVFALTTF	53	R	AF079864.1	632 ... 1576
474	OR5Dn	0	11	51.21	YCVVSGWGVLYLFANEC	48	M	NM_013728.1	1 ... 948
475	OR52Rn	0	11	3.6	VHSSSIRWPFMGVAVAF	58	M	AF121976.2	474 ... 1307
476	ORnP	27	11	51.21	FCFAAGQSPGFLCFFFF	23	M	AB030893.1	37 ... 930

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
477	OR7EnP	6	3	121.47	MVACDVLDLHIIDSFSL	57	M	AF073989.1	547 ... 1515
478	OR6Qn	0	11	54.04	LTGACAVTLPLDVSULA	52	M	NM_010983.1	178 ... 975
479	OR4Fn	0	6	185.89	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
480	OR7EnP	3	13	40.31	FFSP.AAALHIMPAFGL	65	M	X89686.1	32 ... 472
481	OR7En	0	2	95.17	MVACDVLDLHIIDSFGL	57	M	AF073989.1	547 ... 1515
482	OR4Nn	0	14	0.27	LHGAMVGHVQLMNSLSL	58	M	AC019272.4	62255 ... 61317
483	OR2ASn P	7	1	254.77GGGGGMICGLLP	43	M	AF102535.1	16 ... 669
484	OR11Hn	0	14	0.33	FFGTCFIGIPYQSVLF	90	M	AF121972.1	171 ... 1109
485	OR2Tn	0	1	254.77	MLAGFGLDMLIMCCMLI	69	M	AF102527.1	22 ... 669
486	OR2TnP	1	1	254.77	CMMGFSGDLLIMCCMLI	77	M	AF102527.1	22 ... 669
487	OR2AKn P	3	1	254.55	TLGGACSNIHVSGILL	50	M	AF102533.1	16 ... 669
488	ORnP	16	12	4.38	VLKSKCWQLPFYMLLM	25	R	Y07557.1	1 ... 942
489	OR5DnP	4	11	51.21	FCAVTGWSTLFCIANES	48	R	U50948.1	34 ... 978
490	OR7EnP	1	4	5.55	FVACDVLDLHIIDNFG	54	M	AF102536.1	22 ... 669
491	OR5L2	0	11	51.27	FCGVVCCCIHLLVANEV	53	M	AF146372.1	509 ... 1456
492	OR5Dn	0	11	51.27	FCVVLVWCTLSLVANES	48	M	NM_013728.1	1 ... 948
493	ORnP	4	9	81.99	..CCCLFFQSIASGTI	23	M	AL359381.1	82137 ... 81544
494	OR10Qn	0	11	54.08	MVGSCGLPQLLLVSVLI	50	M	AL365336.1	123248 ... 124093
495	OR9MnP	1	11	51.27	LCVDSGGSIHNLFAVEI	54	M	AC069559.8	73704 ... 74636
496	OR7E62 P	5	2	73.96	MAACDVLDLHTIDSFRL	56	M	AF073989.1	547 ... 1515
497	OR9LnP	13	11	54.06	MFVGCTLVAYGILTMIA	32	M	AC069561.1 0	147203 ... 146274

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
498	OR7E46 P	10	2	73.96	MAGVEFCDLHIMPAFGL	54	M	AF102536.1	22 ... 669
499	OR1S1	0	11	54.08	MIVVNILITHLLVGVIF	56	M	AC073769.1	133488 ... 132556
500	OR5DnP	0	11	51.21	FCVIMGWCTLSCISSEC	45	M	AC069563.9	111696 ... 112671
501	OR9InP	4	11	54.06	FTASCGGNICCISAVIT	46	R	AF091579.1	7 ... 663
502	OR5Dn	0	11	51.21	FCVVSGWCELSLLANES	53	M	AF146372.1	509 ... 1456
503	OR9QnP	4	11	54.08	FTASCGASVRTIFAVMA	47	M	AL365337.1	192661 ... 191711
504	OR51Cn P	0	11	3.04	MKTVSARMPMLGAMTVV	51	R	AF079864.1	632 ... 1576
505	OR5WnP	1	11	51.27	FCADCGVDIHL.....	53	M	AC069561.1 0	127636 ... 126698
506	OR9InP	2	11	54.06	FTAGCSCGLHCICAMFA	46	M	AC074177.4	106297 ... 105361
507	OR51An P	4	11	3.04	MHSVSARVPVPGVVTGL	72	M	X89685.1	2 ... 481
508	OR5L1	0	11	51.21	FCVVVCCCIHLLVANEV	55	M	AF146372.1	509 ... 1456
509	OR7EnP	5	13	50.42VVDLHIMPAFGL	66	M	X89686.1	32 ... 472
510	OR5BLn P	18	11	54.08	ILGNXLENQCIFAMIT	29	R	M64392.1	1 ... 942
511	OR51En	0	11	3.04	MHSASVRFPLLGAIVMV	95	R	AF079864.1	632 ... 1576
512	OR51Dn	0	11	3.04	MHSASSRFPLIGIIVMV	61	R	AF079864.1	632 ... 1576
513	OR52In	0	11	3.04	MHTATARFPLMSGSMVS	46	M	AF121975.1	50 ... 1012
514	OR4KnP	2	18	19.04	IHTGMIVHSQFIDSLSS	56	M	AB030896.1	1 ... 906
515	OR52In	0	11	2.99	MHTATARAPLMSGSMVS	47	M	AF121975.1	50 ... 1012
516	OR4KnP	2	18	19.04	IHNGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
517	OR52Mn P	1	11	3.04	MHATSVRYLPIGIGVLL	51	R	AF079864.1	632 ... 1576

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
518	ORnP	7	6	31.58	FLVSCLLLLLLLEGIHW	30	M	AF073964.1	41 ... 649
519	ORnP	9	8	88.25	IXVVVLNIVNMTTIIFL	24	M	AC074177.4	149899 ... 148964
520	ORnP	9	10	70.63	YSIVMFYHAHFICELLN	26	M	AC068902.1 1	144125 ... 143193
521	ORnP	9	9	70.7	WWWWSWYGNFDD SITX	26	R	AF091563.1	7 ... 669
522	ORnP	9	5	202.43	FFFFF.PPPPP.....	27	R	AF034902.1	4197 ... 5177
523	ORnP	10	11	137.77	LLLLWSQFXQFLAVVVV	29	R	M64376.1	1 ... 999
524	ORnP	3	11	16.31	NNNNNLLXMNIILTLLAI	27	M	AL136158.1 4	29455 ... 30402
525	ORnP	17	11	55.6	LAGNNIYCYHM..LLLL	26	R	M64377.1	1 ... 939
526	OR6Pn	0	1	154.6	LIACCASSMKFDLAMIL	60	M	NM_010983. 1	178 ... 975
527	OR7EnP	3	14	33.48	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
528	ORnP	12	11	138.51	LMCHS.FFFFFMMMMM	29	R	AF091573.1	7 ... 663
529	OR7EnP	5	14	33.48	MAGGDFLDLYILPDFGL	55	M	AF073989.1	547 ... 1515
530	ORnP	7	10	127.4	S.CCCLLYIIHHHHHH	31	M	AC020958.1	164590 ... 163746
531	OR10XnP	2	1	154.6	MLGGCSAITELIISGLG	49	M	AC073778.1	168744 ... 167803
532	OR10Zn	0	1	154.71	MAACCTTFGMVILSVLV	56	M	AC025913.3	108128 ... 109067
533	OR6KnP	2	1	154.73	MYGIVGCTPEWVVHEIT	40	R	M64386.1	130 ... 975
534	OR6Kn	0	1	154.73	MHGIVSCTPEWVIHEIT	44	M	AC027184.3	54955 ... 54017
535	OR1FnP	1	4	97.57IEGVMT	73	R	M64377.1	1 ... 939
536	OR1ABnP	3	19	19.44	MIGISAFNTHLV.....	64	M	AC073769.1	133488 ... 132556
537	OR52MnP	1	11	2.89	MHATSARYLPIGIGVLL	49	M	AF121975.1	50 ... 1012
538	OR1XnP	6	5	202.43	MIANTLGIVHIFAALFA	71	M	AF102530.1	1 ... 666

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
539	OR4FnP	8	16	83.04	QQQQQVIHSQFVNSLTC	46	M	AC019272.4	62255 ... 61317
540	OR52Mn P	5	11	2.89	MHATSVRYLPFIGIGVLM	45	R	AF079864.1	632 ... 1576
541	OR2Vn	0	5	209.61	IVVGGSFDIQVICMLF	83	M	AF102535.1	16 ... 669
542	OR2V1P	4	5	209.61	IVVGGSFDIQALCCMLL	90	M	AF102537.1	16 ... 669
543	OR2Zn	0	19	65.55	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
544	OR52Kn P	5	11	2.89AMFIEL	52	M	AF121975.1	50 ... 1012
545	OR10Hn	0	19	19.7	MFGFSWGMVIGLVTAI	75	M	AC023604.2	214343 ... 213396
546	OR2Dn	0	11	5.77	ILGCCRSVVDIFIMGILA	85	M	AF073987.1	2 ... 649
547	OR7EnP	6	2	161.49	VVGGCSSLHIMPAGFL	64	M	X89686.1	32 ... 472
548	OR11Gn P	4	14	0.27	FFGSCSLWIPVSLSLLI	68	M	AC027184.3	54955 ... 54017
549	ORnP	12	14	0.27	GSCGNSLHHYLMVNIIL	28	M	AF121972.1	171 ... 1109
550	OR11Gn	0	14	0.33	FFGSCNLWIPNFLSPVM	67	M	AF121972.1	171 ... 1109
551	OR11Hn P	5	14	0.33	FTGTAFFSVSQFLSIIL	68	M	AF121972.1	171 ... 1109
552	OR6Kn	0	1	154.73	MHENGGFIPEDHATII	46	R	AF034897.1	354 ... 1199
553	OR11Hn	0	14	0.33	FFGTCVGCVPFCFNIIG	71	M	AF121972.1	171 ... 1109
554	OR6KnP	0	1	154.73	MHGNGGFVPEWDHAAIF	46	M	AL365336.1	122764 ... 121784
555	OR11Hn P	2	14	0.33	FFGTCLIGISFFVSFIL	70	M	AF121972.1	171 ... 1109
556	OR6KnP	2	1	154.82	MHGVAGFMPECDRASIT	43	M	AC027184.3	54955 ... 54017
557	OR6Kn	0	1	154.84	MHGISGCLPEWVIHEIA	45	R	AF034900.1	1 ... 963
558	OR2Ln	0	1	254.55	SSGGAGINAHYVSTFLF	53	M	AF102527.1	22 ... 669
559	OR4GnP	8	16	83.04	ICRKMVHSQFVNSISA	45	M	AB030892.1	1 ... 939

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
560	OR6Nn	0	1	154.84	IHGACGGGVELDINKIA	50	R	M64386.1	130 ... 975
561	OR2LnP	2	1	254.55	SLAVGGINAHY.....W	52	M	AF102535.1	16 ... 669
562	OR9A1	0	7	146.91	LLGTLVLSPALMAIIG	45	M	L14567.1	17 ... 667
563	OR6Nn	0	1	155.69	THGACACCSELDINIII	51	M	AL136158.1 4	29455 ... 30402
564	OR10Hn	0	19		MFGFSCGMVVAGLV TAL	86	M	AC023604.2	245345 ... 246298
565	OR7EnP	4	9	71.72	MVACDVLDLHIMNSFGL	57	M	AF073989.1	547 ... 1515
566	OR2AQn P	5	1	155.69	FCHSCLLLLSLLPFFFF	31	M	AL359352.1	55588 ... 56546
567	OR2LnP	3	1	254.55	SMAGAGINAHYVSSFLF	50	M	AF102537.1	16 ... 669
568	OR5ARn	0	11	52.46	FVVD CGASAHLLLCIES	53	R	AF091579.1	7 ... 663
569	OR7EnP	4	9	71.79	TAGGETLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
570	OR10AA nP	2	1	155.69	THGMCAA VPLHVIATC	84	M	AC005992.1 5	9114 ... 8173
571	OR10Jn P	4	1	157.7	MIAICGVVQSNVSVIV	72	M	X92969.1	8035 ... 8961
572	OR5A1P	0	11	55.81	FVGLCGGSIQSNVVVGT	81	M	Y15525.1	1 ... 705
573	OR2AHn P	5	11	52.46	MLGSCISSVILVFSIVI	51	M	AF247657.1	1 ... 945
574	OR10Jn P	4	1	157.7	LLGICGIMVQSNVSVLL	68	M	X92969.1	8035 ... 8961
575	OR56Bn P	2	11	4.93	IHM CSSRLPVLQLVVVS	39	M	AF121975.1	50 ... 1012
576	OR5M1	0	11	52.35	CIVIFIYSSQLMVANLS	49	R	AF091579.1	7 ... 663
577	OR52Wn P	0	11	4.93	MHTASLLAVPLGLSISM	48	M	AF121976.2	474 ... 1307
578	OR5AMn P	5	11	52.35	FIVIYAYNVQLMVANLC	35	M	AC068904.1 5	113793 ... 114719
579	OR52Bn P	3	11	4.93	MHFVSTQTPVLGVPSVV	89	M	AF121975.1	50 ... 1012
580	OR5MnP	1	11	52.35	CVLLYFWVMQLLSANLV	48	R	X80671.1	203 ... 1129

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
581	OR5APn P	6	11	52.35	FGAGGALNIHFIFANES	55	R	X80671.1	203 ... 1129
582	OR56Bn	0	11	4.95	IHFCSFRLPVLQLALVS	41	M	AF121975.1	50 ... 1012
583	OR5APn	0	11	52.35	FGLGCTANIHMIFSIVS	55	M	AF121977.1	262 ... 1197
584	OR52Bn	0	11	4.93	GHFVSARIPVLGVPMVL	73	M	AF121975.1	50 ... 1012
585	OR9Gn	0	11	52.5	FAAYCVGNIIKMLLNVC	45	M	AC074177.4	106297 ... 105361
586	OR52Kn	0	11	2.86	MHSISARLPLLGVASVL	53	M	NM_013619. 1	118 ... 969
587	OR5MnP	1	11	52.35	FIVIYAYNSQLMVANLC	51	M	AC074177.4	106297 ... 105361
588	OR52Kn	0	11	2.86	MHSISARLPLLGVAIVL	52	M	NM_013619. 1	118 ... 969
589	OR52Kn P	3	11	2.82	MHSISARLPLLGVAIGL	53	M	NM_013619. 1	118 ... 969
590	OR52Bn P	4	11	2.78	IHFISARVPDLGVLTVL	57	M	AF121975.1	50 ... 1012
591	OR2B6P	0	6	31.62	LLGAYATNWLLLVSFHI	79	R	L34074.1	73 ... 1011
592	OR2WnP	7	6	31.61	LLRGCASNVMLAFAIVL	58	M	AF102516.1	52 ... 669
593	OR2AnP	5	7	148.83	TMAHCTCLVHLISSILG	72	M	AF102521.1	22 ... 669
594	ORnP	16	6	31.61	FLVSCMDFMYIVLNNVI	39	M	AF102516.1	52 ... 669
595	OR2LnP	0	1	254.55	STAVAGINAHYVSAFLF	50	M	AF102527.1	22 ... 669
596	OR2W2P	5	6	31.61	LLGGCVCQSYWVLSIVM	55	R	L34074.1	73 ... 1011
597	OR2LnP	1	1	254.55	SLAGA.....	61	M	AF102535.1	16 ... 669
598	OR2B7P	1	6	31.61	LLGGCTTNIQLIVSFLV	59	M	AC044846.2	105668 ... 104736
599	OR2Ln	0	1	254.43	SLGGAGINAHYVSAFLF	53	M	AF102527.1	22 ... 669
600	OR5BFn	0	1	254.77	VVVYLASYMHSISAVGG	46	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
601	OR2LnP	4	1	254.55	SVAGMSMDAHYVSTFLF	47	M	AF102527.1	22 ... 669
602	OR7EnP	3	10	17.14	MVACCVLDLHI.....	51	R	AF091580.1	7 ... 663
603	OR1H1	2	9	106.04	LGADNVIHVHLLVALLA	57	M	AC073769.1	133488 ... 132556
604	ORnP	14	1	254.49	TTTKKSERIYIVSSFLI	24	M	AF102527.1	22 ... 669
605	OR4Dn	0	11	55.81	IHGGIASHIQLMNNVTI	64	M	AC019272.4	183633 ... 182701
606	OR1Ln	0	9	106.04	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
607	OR5AXn	0	1	254.2	L TSAIVIFAYGGVGLSS	47	M	AL136158.1 4	154973 ... 155908
608	OR5An	0	11	55.77	YCGLCGGSIESTVSVGV	64	M	Y15525.1	1 ... 705
609	OR5AYn	0	1	254.2	LVAGILNLLYGSIGYAS	50	M	AL359352.1	126933 ... 127889
610	OR13Gn	0	1	255.42	LTLGMMINVHLVADLAG	59	M	AF102540.1	16 ... 669
611	OR5BBn P	0	11	55.77	YASLCGGSVHPLEAVGG	54	M	Y15525.1	1 ... 705
612	OR9GnP	6	11	52.49	FVXNCAGNIIELMLNIT	47	M	AF121977.1	262 ... 1197
613	OR2TnP	4	1	254.77	HLAGFAGNLLVMCCMLI	75	M	AF102527.1	22 ... 669
614	ORnP	7	1	255.42	PVAGKGAFLHSVESLGS	38	M	AL365337.1	192661 ... 191711
615	OR1Jn	0	9	95.9	MITDSVLSSHLMVGUIL	66	M	AF102524.1	52 ... 669
616	OR2CnP	1	16	6.47	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
617	OR9GnP	2	11	52.49	FAAYCYGNILNLLNVS	49	M	AL365337.1	192661 ... 191711
618	OR2C1	0	16	6.4	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
619	OR51An P	2	11	4.22	52	M	AF071080.2	26330 ... 27262
620	OR9Gn	0	11	52.49	LCAYCGGNAHNLVVTVS	53	M	AC068904.1 5	165039 ... 165965

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
621	OR52Bn	0	11	2.78	LHFISTRTPILGILTVL	61	M	AF121975.1	50 ... 1012
622	OR1K1	0	9	105.89	MFGVSMVHLYLIEGVVT	58	R	M64377.1	1 ... 939
623	OR51Rn P	3	11	2.78	MHTYSARLPGLGSISLL	47	R	AF079864.1	632 ... 1576
624	OR7EnP	2	13	54.83	MVACDVLDLHILDSFGL	57	M	AF073989.1	547 ... 1515
625	OR52Pn P	3	11	2.82	MHSASARLPLLGA AVVT	55	M	AF121975.1	50 ... 1012
626	OR7EnP	5	9	70.7	MVACDVQYVHSMDSFGL	48	M	AF102536.1	22 ... 669
627	OR7EnP	5	9	70.7	TAGGD.CCCCC.....	43	M	AF073989.1	547 ... 1515
628	OR4KnP	1	21	8.12	IHTGMIVHSQFIDSLSS	57	M	AF259072.1	104176 ... 105099
629	OR4KnP	2	21	8.12	IHNIGIVVHSQFMTSTAT	54	M	AB030896.1	1 ... 906
630	OR7EnP	6	9	70.7VFLVHVPFAFGL	58	M	X89686.1	32 ... 472
631	OR51In	0	11	4.15	MHSFSGKTPFVG VITYM	51	R	AF079864.1	632 ... 1576
632	OR51In	0	11	4.15	MHSMSGRTPLLGVLT FM	56	R	AF079864.1	632 ... 1576
633	OR2AnP	1	7	148.83	TLAICTFL.....	63	M	AF102521.1	22 ... 669
634	OR2A2	2	7	148.83	TLAVCTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
635	OR2AnP	8	7	148.83	TFAACTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
636	OR2Gn	0	1	256.63	LHGSCMSTVQLLASFLV	59	M	NM_008762.1	1 ... 936
637	OR2AnP	0	7	148.83	TLAHCAFFFFL.....	57	M	AF102521.1	22 ... 669
638	OR6Fn	0	1	254.2	MFGCYGCAVPLAIAVIS	71	R	M64378.1	1 ... 933
639	OR2AnP	4	7	148.83	TLAHCAFLVHLISCILG	68	M	AF102521.1	22 ... 669
640	OR2Gn	0	1	256.02	LLGSCISSIHFLVSEVI	63	M	M84005.1	1 ... 936
641	OR7E37 P	5	13	26.5	MAGGEFLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
642	OR5AVn	0	1	256.02	AMATVMSCMHAVFGLVI	51	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
643	OR2AJn P	7	1	254.43	VLLGCGINVHYVSAFLI	55	M	AF102527.1	22 ... 669
644	OR13En P	1	9	39.89	MLGSCLTNLQLLATLTA	79	M	AJ251155.1	15491 ... 16423
645	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
646	OR2TnP	0	1	254.43	IPGGCSLDLQAMCCMLV	59	M	AF102537.1	16 ... 669
647	OR2WnP	2			LMGSCVCNIMQTLGLLV	56	M	M84005.1	1 ... 936
648	OR13Jn	0	9	39.89	MLGSCALKTEILGSLLV	82	M	AJ251155.1	6062 ... 6997
649	OR6RnP	2	1	254.39	SFGCFLGLPSLDSSLIS	45	M	NM_010983. 1	178 ... 975
650	OR5ATn	0	1	254.39	VLASLVYIMHGLINLDC	50	M	AL359352.1	111313 ... 112242
651	OR2Zn	0	19	10.64	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
652	OR4Ln	0	14	0.08	MHGGMLIHSQVLDSLST	53	M	AB030893.1	37 ... 930
653	OR4UnP	14	14	0.15	RHSGMAMHSQVLDSLST	46	M	AB030895.1	1 ... 924
654	OR4Fn	0	6	185.98	IHGGMIIHIQFVNSISA	50	M	AF102522.1	40 ... 660
655	OR4FnP	2	6	185.98	IHGGMAIHVQFVNSISS	50	M	AB030896.1	1 ... 906
656	OR4Fn	0	6	185.98	IHGGMATHVQFVNSISG	50	M	AB030896.1	1 ... 906
657	OR4Fn	0	6	185.98	IHGGMTIHVQFVNSISG	50	M	AB030896.1	1 ... 906
658	OR4AnP	5	11	50.28	IHGGILGHVQFVNDICV	65	M	AF102522.1	40 ... 660
659	OR4LnP	1	14	0.21	KHGSMLIHSQVLDSLST	53	M	AB030893.1	37 ... 930
660	OR7E33 P	6	13	54.79	MAGGEFLDLRILPAFGL	56	M	AF073989.1	547 ... 1515
661	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
662	OR4Kn	0	14	0.15	MHGGMSVHSQFVDSLST	53	M	AF259072.1	104176 ... 105099
663	OR5U1	0	6	33.45	VIASVAASMHILFTAAI	84	M	AL359352.1	111313 ... 112242
664	OR4Kn	0	14	0.08	IHGGMAVHSQFMDSSLSS	58	M	AF259072.1	104176 ... 105099

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
665	OR5V1	0	6	33.45	LVVGCSANVHLLTGIGT	84	M	AL365337.1	192661 ... 191711
666	OR4QnP	1	14	0.08	LHGAMAGHVQLMNSISI	62	M	AF259072.1	104176 ... 105099
667	OR12D3	0	6	33.45	LHGSAAIYMHMLVTISG	70	M	AL359381.1	128169 ... 127234
668	OR4Kn	0	14	0.08	IHTGMIVHSQFIDSLSS	59	M	AF259072.1	104176 ... 105099
669	OR51CnP	3			MKTVSARMPMLGAMTVV	53	R	AF079864.1	632 ... 1576
670	OR1J2	0	9	105.94	MITDSVLSSHLMVGVL	66	M	AF102524.1	52 ... 669
671	OR5BJnP	3			SIGSAAVNTKFPSC LGV	46	M	AF073965.1	2 ... 643
672	OR1J1	0	9	105.82	TIADSGICLHLIAAAIL	63	M	AF102524.1	52 ... 669
673	OR13En	0			MLGSCLTNLQLLATLTA	83	M	AJ251155.1	15491 ... 16423
674	OR4KnP	5	14	0.08	IHGGMVIHTEFVNSLSM	53	M	AB030893.1	37 ... 930
675	OR1LnP	5	9	105.84	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
676	OR2CnP	2			FHGACAGTVGLMASFVL	59	M	M84005.1	1 ... 936
677	OR4TnP	9	14	0.21	MLSELLSHSQFVKSLSI	47	M	AC019272.4	62255 ... 61317
678	OR5BnP	1			FVITSGCNIHNIVVND F	51	M	AF121977.1	262 ... 1197
679	OR4Kn	0	14	0.21	IHGGMTLHFQFINSISS	53	M	AB030896.1	1 ... 906
680	OR11Ln	0	1	254.43	LVGACVTTLHMILSVLI	50	M	AF121972.1	171 ... 1109
681	OR7E68P	5	10	17.21	MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
682	OR7EnP	2	10	17.21	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
683	OR7E31P	6	9	70.71	TAGGELLDLHIMPAFGL	55	M	AF073989.1	547 ... 1515
684	OR7EnP	3	9	70.71	MVACDVLDLHIMDSFGL	58	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
685	OR5AKn P	3	11	52.82	LAATCGMNVHFLFVNLF	79	R	U50948.1	34 ... 978
686	OR5AKn	0	11	52.83	FAATCGMNVQFLFVNLF	79	R	U50948.1	34 ... 978
687	OR5AKn	0	11	52.83	FAATCGINVFHDFVDLF	79	R	U50948.1	34 ... 978
688	OR5BQn P	9	11	52.82	TTTTTLLLLLMLTFFFF	42	R	U50948.1	34 ... 978
689	OR1Nn	0	9	105.94	LLGGNVLPMLHIMGFLV	56	R	AF091566.1	1 ... 663
690	OR1J4	0	9	105.94	MITDNVLNSHLIVGVIL	69	M	AF102524.1	52 ... 669
691	OR1Nn	0	9	105.94	MLGDSLLVTHLVLGVLV	85	R	AB038167.1	1 ... 933
692	OR2AnP	4	3	94.41	TLAVCTIMVHHLGSIVG	65	M	AF102521.1	22 ... 669
693	OR2ANn P	17	9	93.78VVVLEFMVNLLI	23	M	AC074177.4	128803 ... 129726
694	OR5K1	0	3	104.47	FCETCGAHIHLLFSVQF	51	R	AF091575.1	52 ... 663
695	OR2K2	0	9	93.78	MLGSCVTTLLEFMVSLLI	60	M	AJ251154.1	35662 ... 36615
696	OR8Hn	0	11	51.76	MAGTCGIDVNSIIVTLV	51	M	AC069559.8	36251 ... 35322
697	ORnP	15	11	51.76	LIFKNLFSPLXXHYIL	28	M	X89682.1	2 ... 472
698	OR4AnP	14	11	50.28	FGRRVVGHIQLYGHNYV	38	M	AB030895.1	1 ... 924
699	OR4An	0	11	50.28	LHGGVVGQFQIVNGSCI	59	M	AB030895.1	1 ... 924
700	OR6Sn	0	14	0.58	FFGAFAGPGPADLAVIS	50	R	M64378.1	1 ... 933
701	OR4RnP	16	11	50.28	NLGAIMEHVXSVNGNYL	52	M	AF102522.1	40 ... 660
702	OR13Cn	0	9	86.77	MLGTCGINVQFLTTFLT	65	M	AJ133425.1	61 ... 1014
703	OR13Dn P	4	9	86.77	MYGSCVLNTELIGNFLS	64	M	AC023789.5	371264 ... 372220
704	OR7EnP	3	11	2.13	MIACGVLDLHIINSFGL	54	R	AF091580.1	7 ... 663
705	OR10Pn P	1	12	59.88	MIGICTTTTHLVATFII	49	M	AF247657.1	1 ... 945
706	OR8In	0	11	51.76	MVCCMISISVSLATLS	50	M	AC069559.8	137090 ... 138039
707	OR8G1	0			..IIIGICVHCIVGNIV	75	R	AF091576.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
708	ORnP	7	12	59.88	CFPGEAFFTLL.....	34	M	AL359352.1	145887 ... 145042
709	OR5F1	0	11	51.76	MIATCGANVNHSLANIG	50	M	Y15525.1	1 ... 705
710	OR5FnP	1	11	51.76	MIATCGANVNYFFANKG	52	M	Y15525.1	1 ... 705
711	OR6BnP	6	2	251.7	LSVCCFSIIKFDLAILF	70	M	L14567.1	17 ... 667
712	OR2D1	0			LLGCCASVVDFITGILI	64	M	AF073987.1	2 ... 649
713	OR5ASn	0	11	51.76	MAADCLSTVHLLLCIQS	52	M	AC068904.1 5	165039 ... 165965
714	OR5SnP	8	2	251.7	FSSTTGRSVQLKLCMMN	64	R	AF091579.1	7 ... 663
715	OR5AQn P	0	11	51.76	SAVTDAGNTHGPFESIAF	51	R	X80671.1	203 ... 1129
716	OR6BnP	3	2	251.7	LSVCCFSIIKFDLAILF	67	M	L14567.1	17 ... 667
717	OR5JnP	2	11	51.76	YVLTGGGNTHGLFSIAL	52	R	X80671.1	203 ... 1129
718	OR9AnP	4	7	146.91	QLGTLVFFWPALMAIIG	44	M	NM_010991. 1	1 ... 939
719	OR5BEn P	2	11	51.76	YSLTCVLNTHSFLSTST	45	R	AF091564.1	7 ... 663
720	OR9An	0	7	146.91	LLGTFVFFWPVLMVAVLG	47	M	NM_010991. 1	1 ... 939
721	OR8Hn	0	11	51.76	MVGTCGIDVNSIIATLV	51	M	AC069559.8	36251 ... 35322
722	OR5BNn P	14	11	51.76	LLMTCAYMSHS.....P	54	M	AF102528.1	52 ... 669
723	OR8Jn	0	11	51.76	LLIVVLYTVVCVSANLF	80	M	X89682.1	2 ... 472
724	OR9NnP	9	7	146.91	LFGTFIIIIIL.AAAAA	36	M	NM_010991. 1	1 ... 939
725	OR7EnP	4	7		MVACGMLDLHITHSFAL	51	R	AF091580.1	7 ... 663
726	OR7E9P	3	7		MVACDVLDLHVIDSFGL	51	M	AF073989.1	547 ... 1515
727	OR8KnP	8	11	51.76	MMITLICQIIDILTNP	36	M	AC069563.9	28460 ... 29383
728	OR2AnP	1	7	148.97	ILAHC.....	44	M	AF102521.1	22 ... 669
729	OR8Kn	0	11	51.76	LLIIFIYQMFKSFSNLS	56	M	AF102528.1	52 ... 669
730	OR7E39 P	4			MVGGEFLHLHIMPAFGL	55	R	AF091580.1	7 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
731	OR7E27P	3			MAGGELLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
732	OR2Hn	0	6		FLGTCVMEVQSLASILV	81	M	AL078630.1	41097 ... 40165
733	OR13CnP	2	9	40.16	MLGACGATVQLMANFLV	87	M	AJ133428.1	61 ... 1017
734	OR13Cn	0	9	40.16	MFGACGAAVQLMTNFLV	89	M	AJ133424.1	61 ... 1017
735	OR2S1P	4	9	40.16	MFGACGANVQLMTNFLL	89	M	AJ251154.1	2703 ... 1747
736	OR2AMnP	1	9	40.16RRRRRV.MMMMM	63	M	AJ251154.1	2703 ... 1747
737	OR1N1	0	1		MLGDSLLVTHLVLGVLV	85	R	AB038167.1	1 ... 933
738	OR2S2	0	9	40.13	MFAGCSIAVHLMTNFLV	83	M	AJ251154.1	2703 ... 1747
739	OR7E26P	4	1		MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
740	OR1F11	0			LAGNNGVNLHLIEGVM	99	R	M64377.1	1 ... 939
741	OR5ACnP	3	3	103.97	FGATCIIHIHLIFSIOF	66	R	AF091575.1	52 ... 663
742	OR5B10P	2	13		MVATNGCNLRDLMSNV	46	M	AF102528.1	52 ... 669
743	OR2AnP	1	12	85.7	TLAVCAFLVHLIACILG	76	M	AF102521.1	22 ... 669
744	OR1E5	0	13		MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
745	OR4Fn	0	6	185.71	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
746	OR5CnP	0	9	40.53	MAADC.....	47	M	Y15525.1	1 ... 705
747	OR2WnP	0	6	31.62	LLGGCVSNIMQALAIIA	64	M	AF102516.1	52 ... 669
748	OR2L2	0			..IIIGINAHYVSSFLL	48	M	AF102537.1	16 ... 669
749	OR4H8P	2	14		MHGCI LGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
750	OR5D10P	5			LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
751	OR7A12P	1	14		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
752	OR2L1	0			..IIIGINAHYVSTFLF	48	M	AF102527.1	22 ... 669
753	OR2F3P	0	14		LLGGFTSSVQIISSLLT	55	M	AF073974.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
754	OR4H10 P	2	15		MHGCI LGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
755	OR5H1	0			..IIILGHIHFVFSIQF	56	R	AF091575.1	52 ... 663
756	OR2K1	0			..IIIITTLVCMVSLLI	58	M	AJ133428.1	61 ... 1017
757	OR7E11 P	7	11		MAGGEFLDLHILPAFGL	52	M	AF073989.1	547 ... 1515
758	OR7A3P	1	11		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
759	OR6A1	0	11		LLGCCGGIVKLDLAILG	91	R	M64386.1	130 ... 975
760	OR5I1	0	11		FCADSLGSHVFLYGVEI	52	M	Y15525.1	1 ... 705
761	OR2H3	0	6		ILGTCVIGVQSVASILV	86	M	AL078630.1	41097 ... 40165
762	OR10J1	0			MVGICGIVTQSTISVLV	73	M	X92969.1	8035 ... 8961
763	OR7E3P	3	11		MFACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
764	OR1D6P	1	11		LVVANLFYIHLLTGIFI	48	R	Y07557.1	1 ... 942
765	OR5D10 P	2	18		LCVTTWCTLFTSASES	45	R	U50948.1	34 ... 978
766	OR5D5P	2	18		LCVTTWCTLFTSANES	46	M	AC073947.3	29192 ... 30115
767	OR52A1	0	11		MHQGSMVCLIGVAVAF	72	M	NM_013620. 1	1 ... 945
768	OR2AEn	0	7	98.36	HLGGCMGNIHIVSSLLL	48	M	AC073769.1	143294 ... 142353
769	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	40	M	NM_010983. 1	178 ... 975
770	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	41	M	NM_010983. 1	178 ... 975
771	OR7MnP	7	10	149.44NVYVSL.....	29	M	AC073947.3	43325 ... 42733
772	OR13Cn	0	9	86.77	MFGACGTDVQFMSNVLI	69	M	AJ133428.1	61 ... 1017
773	OR13Cn	0	9	86.85	MLGTCGANVQFMATFTM	71	M	AJ133425.1	61 ... 1014
774	OR2InP	6			LLGSC.....	79	M	AL078630.1	151152 ... 150391

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
775	OR4An	0	11	50.28	LHGGVVGHFQVVNSICV	58	M	AB030895.1	1 ... 924
776	OR2InP	3		RRRRRMARILL	77	M	AL078630.1	151152 ... 150391
777	OR4AnP	4	11	50.28	LHGGVVGSGFQVVNGICV	53	M	AB030896.1	1 ... 906
778	OR4AnP	7	11	50.28	PHGGAVAHFQVVNGICV	57	M	AB030896.1	1 ... 906
779	OR8C1P	2	11		LCVHCGMGVHCMIVVVV	72	M	AC068905.1 2	76922 ... 75948
780	OR4AnP	1	11	50.28	LHGDVVGHFQVVNGICV	56	M	AB030896.1	1 ... 906
781	OR7E15 P	5	11		MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
782	OR10A1	0	11		MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
783	OR2An	0			TSAVCTCLVHLI.....	70	M	AF102521.1	22 ... 669
784	OR7EnP	6			MAGGELFHLHIMPAFGL	57	M	AF073989.1	547 ... 1515
785	OR7En	0			MAGGDFLDLHIVPAFVL	54	R	AF091580.1	7 ... 663
786	OR51A1 P	5	11		MHTLSARLPLLAVITFL	43	R	AF079864.1	632 ... 1576
787	OR7E47 P	4			KAGTNLLDLYIMPTFGL	56	M	AF073989.1	547 ... 1515
788	OR5B5P	2	3		MAATNICNIHELVANIS	48	M	AF146372.1	509 ... 1456
789	OR1F10	0	3		MFVDNGVNLHLIEGVM	72	R	M64377.1	1 ... 939
790	OR8G2	0			..IIIGLGIHFVLSNIT	75	M	AF102518.1	52 ... 669
791	OR1Sn	0	11	54.08	MIVVNILITHLLVGVIF	55	M	AC073769.1	133488 ... 132556
792	OR4AnP	3	11	50.73	LHGGAVGHFQVVSGLCV	56	M	AB030896.1	1 ... 906
793	OR4AnP	7	11	50.76	LHGGILGHFQVVNGMCV	58	M	AB030896.1	1 ... 906
794	OR4AnP	5	11	50.66	LHGGVLGHFQVVNGMRV	56	M	AB030896.1	1 ... 906
795	OR4AnP	7	11	50.73	PHGGVVGGRFQVVKVICV	54	M	AB030896.1	1 ... 906
796	OR4AnP	1	11	50.81	LHGGIVGHFQVVS GMCV	60	M	AB030896.1	1 ... 906
797	OR4AnP	10	11	50.81	LHGGVVGNGFQVVNGICV	55	M	AF102522.1	40 ... 660
798	OR4An	0	11	50.73	LHAGVAGHVQFMNGICV	62	M	AB030895.1	1 ... 924
799	OR4An	0	11	50.73	LHGGVVGHVQFVNGICV	57	M	AB030896.1	1 ... 906
800	OR7E42 P	4			MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
801	OR2M3P	2			ITLGCFLDIDALCCMIF	55	M	AF102537.1	16 ... 669
802	OR4H11P	2	4		MHGCILGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
803	OR7E57P	5			MAXGEFLDLHILPAFGL	51	M	AF102536.1	22 ... 669
804	OR2B1P	0	5		LLGAYATNWL LLSVFHI	78	R	L34074.1	73 ... 1011
805	OR7E34P	2			MAGGDSL DLHIMPAFGL	56	M	AF073989.1	547 ... 1515
806	OR7E56P	4			MAGDELFFLHILPAFGL	52	M	AF073989.1	547 ... 1515
807	OR3AnP	1	5		LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
808	OR4H5P	2	5		MHGCILGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
809	OR1En	0	5		MLGDSLLHLHLIMGILI	82	R	Y07557.1	1 ... 942
810	OR51CnP	2	11	3	MKTVSYYYIXQ.....	48	M	AF121975.1	50 ... 1012
811	OR2WnP	2	6	30.51	LLGGCVSNIMQALAIIA	64	M	AF102516.1	52 ... 669
812	OR51B1P	5	11		AHSVSGRSPVRPLITIL	68	M	AF071080.2	15931 ... 16851
813	OR7E81P	3			MAGGEFFSLHIMPAFGL	54	M	AF102536.1	22 ... 669
814	OR7E44P	1			MAGGELFDLHIMLAFGL	53	M	AF073989.1	547 ... 1515
815	OR5B7P	2	6		MAATNICNIHELVANIS	47	M	NM_013728.1	1 ... 948
816	OR7E36P	4			MAGGELFFLHIMPAFGL	58	M	AF073989.1	547 ... 1515
817	OR2A5	0	7		TMAHCTCLVHLIASILG	74	M	AF102521.1	22 ... 669
818	OR5B1P	2	8		MAATNICNIHELVANIS	47	M	AF146372.1	509 ... 1456
819	OR8B8	0	11	137.68	LLVVSGMGAHCVVVDIV	72	M	AC069559.8	120212 ... 119283
820	OR8B4P	0	11	137.71	LCVNCGVGAHSFVVITL	87	M	AC068910.2	133103 ... 132162

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
821	ORnP	15	11	137.77	LCVENRRRTATHCKSHII	35	M	AC069563.9	60295 ... 59327
822	OR8B3	0	11	137.77	LLVICAMGAHCVVNVIV	85	M	AC069563.9	129775 ... 130725
823	OR2Bn	0	6	30.51	LLGSCASNLOWLISFLI	89	R	L34074.1	73 ... 1011
824	OR8B6P	6	11	137.77	LAFFCGLSAHCVAAVI	73	M	AC069559.8	96224 ... 95292
825	OR8B5P	6	11	137.77	LFFFXGLGAHCVVANTV	73	M	AC069559.8	96224 ... 95292
826	OR4E2	0	14	1.7	LHACIAGHGQLINSISS	90	M	AF259072.1	104176 ... 105099
827	OR8B7P	4	11	137.77	FCVICGWGAHCVAAIFV	71	M	AC069559.8	96224 ... 95292
828	OR11JnP	3	15	1.82	FSCAGFGSMPLCVSIII	56	M	AF121972.1	171 ... 1109
829	OR4E1P	3	14	1.7	MHACIAGHALLINSISV	92	M	AB030893.1	37 ... 930
830	OR10DnP	7	11	137.96HHHILLGNVLSI	85	M	AC074177.4	12106 ... 13038
831	ORnP	10	14	1.7	VFRGGFHKFFF.....	23	M	AF102536.1	22 ... 669
832	OR8D2	0	11	137.77	LLVIGVLVWVHRLIGNTA	70	M	AC073947.3	29192 ... 30115
833	OR11InP	1	1	126.31	FGAACGCLITLATSVTI	51	M	AL359381.1	175785 ... 176720
834	OR11JnP	1	15	1.82	FSCACFGWTPLCISII	56	M	AF121972.1	171 ... 1109
835	OR10AnP	3	11	5.64	MFGVCTPVVQWAGTVVI	74	M	AF247657.1	1 ... 945
836	OR8C3P	5	11	137.77	LCVHCGMGVHCMIVVVV	73	M	AC068905.1 2	76922 ... 75948
837	OR2DnP	6	11	5.64	LLGCCGSVVDFITGILI	62	M	AF073987.1	2 ... 649
838	OR4PnP	0	11	51.03	LHGGIVGHSQL.....	59	M	AB030895.1	1 ... 924
839	OR7E21P	5			MAGGEFIDLHIMPAFGL	50	M	AF073989.1	547 ... 1515
840	OR2M1	0			IVLGCFLDIYAICSMFLF	55	M	AF102537.1	16 ... 669
841	OR7AnP	4	19		NLAGVVMNLQM.....	63	M	AF073970.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
842	OR5D11 P	1	8		LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
843	OR7E50 P	7	8		IVVCDMLDLHVFLDIFL	57	M	AF102536.1	22 ... 669
844	OR7E45 P	3			MAGGELFDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
845	OR7E77 P	6			MAGGEFLDLHIMPAFGL	51	M	AF073989.1	547 ... 1515
846	OR8B2	0	11	137.77	LLVICAMGAHCVVVNIV	84	M	AC069563.9	129775 ... 130725
847	OR8D1	0	11	137.77	LVVVGALSTHALIANTV	87	M	AC073947.3	29192 ... 30115
848	OR8B1P	4	11	137.77	LLLVCGMGAHCVVVNIV	84	M	AC069559.8	96224 ... 95292
849	OR7A1P	2	19		MIVVSVVYLQMMTSLGG	72	R	M64376.1	1 ... 999
850	OR7E8P	4	8	13.72	MVACGVLDLHIIDSFGL	53	M	AF102536.1	22 ... 669
851	OR4DnP	7	11	55.86	MHGGVAGHVQLMNNISL	58	M	AC019272.4	183633 ... 182701
852	OR7E80 P	7	8	13.72	MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
853	OR4DnP	5	11	55.86	MHGGGAAGHVQLMNNLTL	62	M	AC019272.4	183633 ... 182701
854	OR7E10 P	8	8	13.72	IVACDLLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
855	OR10B1 P	3	19	17.91	MLGCCLSVIEMILSVVM	85	M	AC012302.5	54283 ... 55224
856	OR2InP	3		LLLLMARILL	75	M	AL078630.1	151152 ... 150391
857	OR4Dn	0	11	55.86	MHGGVGGHAQLMNNVSF	65	M	AC019272.4	183633 ... 182701
858	OR5ACn	0			.VVVVIIHVHLIFGIQP	65	R	AF091575.1	52 ... 663
859	OR2I1	0	6	33.63	LLGSCASNAQLMARILL	79	M	AL078630.1	151152 ... 150391
860	OR10H1	0	19	19.86	MFGFSCGMVVAGLVTAL	88	M	AC023604.2	245345 ... 246298

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
861	OR7E59 P	5			CPEARVFLHIMPAFGL	53	M	AF102536.1	22 ... 669
862	OR7E28 P	4			MAGGELLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
863	OR5B3	0			MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978
864	OR2A6	0			TLAHCAFLVPLIACILG	75	M	AF102521.1	22 ... 669
865	OR6Cn	0			.VVVVCAIPPLVMAALI	47	M	NM_010991.1	1 ... 939
866	OR7E54 P	5			MAGGEFLDLHIMPAFGL	52	M	AF073989.1	547 ... 1515
867	OR7E48 P	3			MAGGEFLDLHIMPAFGL	57	R	AF091580.1	7 ... 663
868	OR67An P	3	11	76.42	MHSCAGTLPAQGIAVSL	83	R	AF091561.1	52 ... 663
869	OR4Dn P	1	11	55.86	MHGGVAGHVQLMNNLTL	63	M	AC019272.4	183633 ... 182701
870	OR4Cn P	1	11	50.91	VHGCILGHAQLLSICS	57	M	AB030896.1	1 ... 906
871	OR4Dn P	2	11	55.86	IHGGIAGHVQLMNNVTL	65	M	AC019272.4	183633 ... 182701
872	OR10H2	0	19	19.94	MFGFSCGMVVAGLVMAL	85	M	AC023604.2	245345 ... 246298
873	OR10H3	0	19	19.94	MFGFSWGMVMGLVTAI	75	M	AC023604.2	214343 ... 213396
874	OR55Cn P	2	11	2.65	VYLLYLQPGGG.....	45	M	AF121980.1	160 ... 1053
875	OR55Bn P	3	11	2.65	.VVVVLQVPLLGMCTVS	53	M	AF121980.1	160 ... 1053
876	OR52Vn P	4	11	4.19	LHNHIMVYXFLGTTSP	48	M	NM_013619.1	118 ... 969
877	OR2B3	0	6	33.64	LLGACFINLQLFSILI	75	R	L34074.1	73 ... 1011
878	OR52Tn P	6	11	4.22	FGHFLIFLDFLDILTIS	45	M	AF121975.1	50 ... 1012
879	OR2J1P	5	6	33.64	LLGTCASTLHFLMSFVI	57	R	L34074.1	73 ... 1011
880	OR52Hn P	3	11	4.19	LHFVSGRVPCLGVPTVT	60	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
881	OR2J3	0	6	33.64	LLGTCASNLHFLTSFVI	58	R	L34074.1	73 ... 1011
882	OR52An	0			FHSVS.....VVRLFS	75	R	AF079864.1	632 ... 1576
883	OR4Qn	0			.VVVVAGHMQLVNSLSV	56	M	AB030893.1	37 ... 930
884	OR52Bn P	2	11	4.22	LHFVSVRTSILGVPSVL	60	M	AF121975.1	50 ... 1012
885	OR2N1P	9	6	33.64	LHGGCPIYSEALVCMLV	81	M	AJ132195.1	79 ... 906
886	OR51En P	1			FHSASVRFPLLGAIAMV	90	R	AF079864.1	632 ... 1576
887	OR2J2	0	6	33.64	LLGICAIILHFLMSFVI	57	R	L34074.1	73 ... 1011
888	OR2In	0		RRRRRRMARILR	77	M	AL078630.1	151152 ... 150391
889	OR2J4P	5	6	33.64	LLGTCASNLHFLTSFVL	56	R	L34074.1	73 ... 1011
890	OR7E40 P	4			MAGGDILDLYILPDFGL	55	M	AF073989.1	547 ... 1515
891	OR2H4P	3	6	33.64	LLGAYLTQIQAMASLLM	63	M	AL078630.1	41097 ... 40165
892	OR7E52 P	5			IVVCDVLDLHVCDIFGL	61	M	AF073989.1	547 ... 1515
893	OR2InP	9			LLGSC.....	80	M	AL078630.1	151152 ... 150391
894	OR6C1	0			LIGVFTVIPALGCATLF	52	M	NM_010991. 1	1 ... 939
895	OR7E30 P	3			MAGGEFLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
896	OR5BAn P	0	11	53.69	LVVTSVFNIQNLFVTL	51	R	AF091579.1	7 ... 663
897	OR7H1P	3	19	11.38	MMGGTVLYIQLLVALDV	74	M	AF073989.1	547 ... 1515
898	OR5B2	0	11	54.45	MVATNGCNFHLTSNIF	47	R	U50948.1	34 ... 978
899	OR5AZn P	1	11	53.69	MIGTCTVNLLCILCLIF	48	R	AF091579.1	7 ... 663
900	OR5Bn	0	11	54.45	MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
901	OR52Bn	0	11	4.22	KILFSARIPSLGAASTL	64	M	NM_013619.1	118 ... 969
902	OR5BnP	2	11	54.45	MAATNICNIHELVANIS	49	R	U50948.1	34 ... 978
903	OR52Dn	0	11	4.19	MHYASVRIPFLGVAAML	66	M	AF121976.2	474 ... 1307
904	OR7A11	1	19	17.72	MVEASAIIDLHMAVLGV	67	M	AF283558.1	1 ... 927
905	OR5BnP	9	11	54.45	MAATSALTVDDLQFFL	41	M	NM_013728.1	1 ... 948
906	OR51AnP	5	11	4.19	THSWFSRMPPLLGIVAFV	50	R	AF079864.1	632 ... 1576
907	OR7A15P	4	19	17.72	MIVGSVTHLHMMALGG	74	R	M64376.1	1 ... 999
908	OR7C2	0	19	17.72	IIGCNGIGLETMTLGF	98	R	AF091580.1	7 ... 663
909	OR7E23P	7	21	20.89	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
910	OR2E1	8	6	32.05	AHACCTINLQI.RRRRR	43	M	AL078630.1	106872 ... 105934
911	OR1I1	0	19	17.87	MHGTSAIQIHLIFGVGS	57	R	AF091566.1	1 ... 663
912	OR1RnP	3	17	3.12	MVGISAVHLHLIEGVVA	45	R	M64377.1	1 ... 939
913	OR4F3	0	8	0.07	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
914	OR2AEn	0	7	98.7	HLGGCMGNIHIVSSLLL	49	M	AC073769.1	143294 ... 142353
915	OR2InP	7		TTTTMARILL	72	M	AL078630.1	151152 ... 150391
916	OR52AnP	2			IHSASVRFPPLGXPPPP	94	R	AF079864.1	632 ... 1576
917	OR7C1	0	19		ITGCNGIGLETIATLGI	81	R	AF091580.1	7 ... 663
918	OR2A3P	2	7	149.11	MLAACTCLINLVGGVLG	63	M	AF102521.1	22 ... 669
919	OR7A5	0	19		MIAGNAMYLMITVLGG	74	M	AF283558.1	1 ... 927
920	OR2InP	3		MARILL	67	M	AL078630.1	151152 ... 150391
921	OR7A10	0	19		MLVGNAMNLQMMAVLGG	76	R	M64376.1	1 ... 999
922	OR2An	0			81	M	AF102521.1	22 ... 669
923	OR2M2	0			IISGCFLDIDAICCMFLF	57	M	AF102537.1	16 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
924	OR7A8P	2	19		MLAVSSSLNLQMIATLGG	71	M	AF283558.1	1 ... 927
925	OR2An	0			TSAVCTTLIHL.....	78	M	L14566.1	62 ... 667
926	OR7E20P	4			MAGGELLFLHIMPAFGL	56	M	AF073989.1	547 ... 1515
927	OR2AnP	3			TLAHTCLVHL.....	65	M	AF102521.1	22 ... 669
928	OR5BHn P	7			MVASCGGKTVS.....	34	M	Y15525.1	1 ... 705
929	OR1En	0			LMGDSLLHLHLIMGISI	92	M	AC068902.1 1	196434 ... 195499
930	OR1EnP	1			MLGDSLLHLHLIIGVVL	98	M	AF073976.1	32 ... 649
931	OR5Bn	0	11	54.45	FVITSGCNIHNIVVNDP	51	R	U50948.1	34 ... 978
932	OR8Rn P	12	11	73.74	LFLSYGGGAHH.....	52	M	AC069561.1 0	7848 ... 8783
933	OR5ANn	0	11	55.69	YSGLSGTAFQATLTFGA	55	R	AF091564.1	7 ... 663
934	OR5ANn P	1	11	55.69	YSGLCGTGIQATLTFGT	59	M	Y15525.1	1 ... 705
935	OR5BRn P	8	11	55.69	MSNVCGTVIQATLTFGT	33	M	Y15525.1	1 ... 705
936	OR2A1	0	7	149.18	TLGHCTCLAHLIACFLG	77	M	AF102521.1	22 ... 669
937	OR10An	0	11	6.81	MLGGCFLLVQWAGTIIV	54	M	AF247657.1	1 ... 945
938	OR2A9	3	7	149.18	TLAHTCLVHLIACILG	78	M	AF102521.1	22 ... 669
939	OR2A7	0	7	149.18	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
940	OR10A3	0	11	6.81	MLGGCFSVVQWAGTIVV	58	M	AF247657.1	1 ... 945
941	OR10Cn	0	6	33.36	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
942	OR7A2P	0	19		MVIVSVMNLQVMAALDG	73	M	AF283558.1	1 ... 927
943	OR10Wn P	2	11	54.3	MIGSCASLQLFVAAAIV	47	M	AC012302.5	54283 ... 55224
944	OR7A17	0	19		MVGGSAINSQMMALAG	76	M	AF283558.1	1 ... 927
945	OR5Bn	0	11	54.3	MAATNGINIQDLISNVF	47	M	AF102528.1	52 ... 669
946	OR5BnP	5	11	54.3	MVATNGCNLRDLMSNVL	47	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
947	OR1Q1	0	9	106.13	TIAVNMLHLHLIEGVIG	54	M	AF073967.1	2 ... 649
948	OR2Hn	0	6	33.33	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
949	OR7EnP	5	3	90.04	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
950	OR7A14	0	19	17.72	MVIVSAMNI.....	71	M	AC073772.1	227187 ... 226252
951	OR1B1	0	9	106.13	FYGVTLVHLRLIEGLMG	49	M	AC068902.1 1	83719 ... 84647
952	OR12D2	0	6	33.23	LHGSSTIHLHMLVTIAG	81	M	AL359381.1	105330 ... 104407
953	OR7EnP	4	3	11.92	MVACDVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
954	OR8BnP	5	15	74.31	LXVVEGMAHCVVVNIV	82	M	AC069559.8	96224 ... 95292
955	OR1L1	0	9	106.13	MLGNSLIHLHLVEGVIT	57	M	AC023167.7	60743 ... 61663
956	OR11An	0	6	33.36	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
957	OR7AnP	4	12	44.29HLLDCYIRTTLSG	55	M	AF102534.1	52 ... 669
958	OR1C1	0	1	254.35	LVVNSGVHLHLIVGLAT	56	M	AC073769.1	133488 ... 132556
959	OR1D2	0	17	2.99	LVVANLLYIHLTGTIFI	50	M	AF073967.1	2 ... 649
960	OR1L3	0	9	106.13	MLGNSFFHLHLAEGSVA	53	M	AC023167.7	14677 ... 15636
961	OR12Dn P	1	6	33.36	LHGSATIHLHMSTGIAG	76	M	AL359381.1	105330 ... 104407
962	OR4G1P	4	16	83.04	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
963	OR2B4P	1	6	33.53	LLGSCGSNVQLLLGLLM	90	M	AL359352.1	95024 ... 95965
964	OR11H1	0	22		FFGTCLCWIPLCLSVIG	61	M	AC027184.3	54955 ... 54017
965	OR4Fn	0	16	83.04	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
966	OR56An P	5	11	4.73	MNLPSFQLPVLQAGFLS	38	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
967	OR8NnP	7	4	164.13	REIIRVDAFLKKTANMI	34	M	AF102528.1	52 ... 669
968	OR7EnP	5			MVACDVLDLHIFDFGL	54	R	AF091580.1	7 ... 663
969	OR4Pn	0	11	50.95	LHGGIVGHSQVLNSIAV	56	M	AB030895.1	1 ... 924
970	OR6Cn	0			LIGVFCSTPPLGFATLF	51	M	NM_010991.1	1 ... 939
971	OR5BCnP	2	11	54.3GCQIHFLLANIF	41	M	AC069561.10	51687 ... 50743
972	OR10QnP	4	11	54.3	MLGGCGLLQLLVSVLV	48	M	AC012302.5	54283 ... 55224
973	OR5BnP	6	11	54.3	TDASNGGNIHELVTNIF	45	R	U50948.1	34 ... 978
974	OR10PnP	2	12	115.61	MIGICTTTTHLVATFII	46	M	AF247657.1	1 ... 945
975	OR1L4	0	9	106.22	MMGNSGIHFRLVETVIT	62	M	AF073967.1	2 ... 649
976	OR2APnP	3	12	115.61	YMGAFLLLLLL.....	49	M	AF073987.1	2 ... 649
977	OR1L6	0	9	106.22	MMGNSGIHFRLVETVIT	63	M	AF073967.1	2 ... 649
978	OR6UnP	6	12	115.61	DIGAFTLFMPLDLAALG	52	M	NM_010991.1	1 ... 939
979	OR5C1	0	9	106.06	MAADCAGSVHLLICIQA	50	R	X80671.1	203 ... 1129
980	OR11InP	1	15	70.72	FGAACGCLITLATSVTI	51	M	AL359381.1	175785 ... 176720
981	OR4AnP	6	11	50.78	LYGGVVGHFQVVGVCV	57	M	AB030896.1	1 ... 906
982	OR4GnP	14	2	114.45	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
983	OR10Vn	0	11	56.15	MVGCGLLPLLLISVLI	48	M	AL136158.14	29455 ... 30402
984	OR4G2P	2	2	114.45	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906
985	OR10VnP	3	11	56.15	MIGRCGLLQLLMVSVLV	45	M	X92969.1	8035 ... 8961
986	OR4F4	0	2	114.45	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
987	OR4G3P	14	19	63.51	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
988	OR5AKnP	4	11	52.82	LGATCSMNINFLFVNLC	65	R	U50948.1	34 ... 978
989	OR10YnP	14	11	56.15	MIRGCGLLFLLLCGHHL	43	M	AF247657.1	1 ... 945
990	OR4GnP	2	19	63.51	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
991	ORnP	9	5	111.92	IMCSRTTYVXQLHGFFT	23	M	AF073989.1	547 ... 1515
992	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
993	OR8A1	0	11	137.56	LLVICVIGIELVSANIV	61	M	AC069559.8	96224 ... 95292
994	OR8Bn	0	11	137.56	LCVVSGMGAHSVVDVM	66	M	AC069559.8	120212 ... 119283
995	OR6DnP	3	10	47.91	AYVSSLLLRTH.....	55	R	AF034901.1	2110 ... 3078
996	OR7E14 P	7	11	16.31	MAGGELLDLHIMPAFGL	58	R	AF091580.1	7 ... 663
997	OR2M4	0			IVLGCALDIVALCCMLF	57	M	AF102537.1	16 ... 669
998	OR4WnP	3	X		LLLLL.....LLFFII	36	M	AC069559.8	73704 ... 74636
999	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
1000	OR7EnP	3			MAGGESLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
1001	OR4GnP	4	19	63.51	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
1002	OR10Jn P	1			LLGVCGITIQSTISVLL	60	M	X92969.1	8035 ... 8961
1003	OR52En	0	11	4.58	MHTASIRMPLLGNIILL	71	M	AF121979.1	53 ... 1106
1004	OR4RnP	24	11		VHGAIMGHVXSFANNCL	54	M	AF102522.1	40 ... 660
1005	OR4Cn	0	11		AHGAIVGHIQFVNSICL	75	M	AF102522.1	40 ... 660
1006	OR4AnP	10	11		GLGGIVGHIQL.....	44	M	AF102522.1	40 ... 660
1007	OR4AnP	4	11		LHGGVAGHFQVVNGGCI	55	M	AB030895.1	1 ... 924
1008	OR4AnP	8	11		LHGGVAGHSHSVNGICV	54	M	AF102522.1	40 ... 660
1009	OR9Gn	0	11	52.54	FAAYCVGNIIKMLLNVC	46	M	AC074177.4	106297 ... 105361
1010	OR10An	0	12	59.65	MFGSCGSVLQWASTFIF	64	M	AF247657.1	1 ... 945
1011	OR4Cn	0	11		VHRGVVGHIQFINSICL	73	M	AF102522.1	40 ... 660

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1012	OR10Vn P	8	11	56.15	.FFFFIIXNEXSVVVLV	37	M	AC073945.4	110931 ... 111893
1013	OR10Un P	3	12	59.65	MAGLCATVAQLMLSFIS	56	R	AF034898.1	1 ... 981
1014	OR7E2P	3	11	90.37	MVACDVLDLHICDIFGL	59	M	AF073989.1	547 ... 1515
1015	OR7E35 P	6	4	11.87	MAGGEFLDLHIVPAFVL	53	M	AF102536.1	22 ... 669
1016	OR9KnP	0	12	59.71	LAIVGGCSLQVSLSIIP	49	R	AF091579.1	7 ... 663
1017	OR7E13 P	5	11	90.37	MAGGEFLDLHIMLAFGL	54	R	AF091580.1	7 ... 663
1018	OR7EnP	4	8	6.5	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
1019	OR9Kn	0	12	59.71	LAIVGGCSIQMSLSIIP	49	M	NM_013728. 1	1 ... 948
1020	ORnP	13	11	137.56	PCVIYGIDVHSLXEPAY	34	M	AC069559.8	36251 ... 35322
1021	OR7EnP	8	11	72.11	MAGGNLFFSLLMPAFGL	54	M	AF073989.1	547 ... 1515
1022	OR7EnP	5	3	140.64	MAGGKFLDLHIMPAFGL	53	M	AF073989.1	547 ... 1515
1023	OR3A4P	0	17	3.12	LHAGCMFNTQALAAMGA	44	M	AC073769.1	133488 ... 132556
1024	OR8QnP	9	11	137.56	LSIIIVETEFVFTXIVT	33	M	AC069559.8	137090 ... 138039
1025	OR7EnP	2	11	72.11	ILACGVLDLHIMHNFGL	55	M	AF073989.1	547 ... 1515
1026	OR7EnP	3	3	140.64	MVACGVLDLHIHSFGL	56	M	AF073989.1	547 ... 1515
1027	OR3A1	0	17	3.07	LHVGCACNTHALVGMAT	50	M	AF073967.1	2 ... 649
1028	OR5Gn	0	11	52.52	MGEACGMSTHFLAIGL	69	M	AF146372.1	509 ... 1456
1029	OR5MnP	7	4	42.45	LIIIYVYNAQRIIIMLE	39	M	AF073987.1	2 ... 649
1030	OR7EnP	1	3	136.02	MVACDVLDLHIIDNFGL	54	M	AF073989.1	547 ... 1515
1031	OR5G1P	2	11	52.51	QGVACGINTHNVVAVGF	68	M	AF146372.1	509 ... 1456
1032	OR5PnP	3	11	6.93	LVGTCAGNSFCPSSVLS	70	M	AF121977.1	262 ... 1197

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1033	OR10AEnP	8	1	157.36	IIIIIGIMVIVQIHCVV	40	M	X92969.1	8035 ... 8961
1034	OR3A2	0	17	3.07	LHAGCACNTHALVGMAT	50	M	AC073769.1	133488 ... 132556
1035	OR10Jn	0	1	157.4	MVATCGIMLHANVSVIV	88	M	X92969.1	8035 ... 8961
1036	OR1D3P	2	17	2.94	LVVANLFYIHLTLTGIFI	50	R	Y07557.1	1 ... 942
1037	OR10Jn	0	1	157.36	TVAICGIMVQSNVRVIV	72	M	X92969.1	8035 ... 8961
1038	OR1D4	0	17	2.99	LVVTNLLYLLLLTGIFT	49	R	Y07557.1	1 ... 942
1039	OR5GnP	8	11	52.51	QGVVYVANTHAVVAVLV	55	M	NM_013728.1	1 ... 948
1040	OR4SnP	1	11	50.99	LHGCIGGHIQLVNSIAG	61	M	AB030895.1	1 ... 924
1041	OR5GnP	4	11	52.51	LGVVCGVSTHFLVLGL	75	M	AF146372.1	509 ... 1456
1042	OR9HnP	2	1	254.35	FSGIAGWNAQMLLCIIS	59	R	AF091579.1	7 ... 663
1043	OR1A1	0	17	2.99	MIGNSGINPHLMGVIFV	86	M	AF073966.1	41 ... 643
1044	OR1A2	0	17	2.99	MIAKSGISPHMLGVFL	80	M	AF073966.1	41 ... 643
1045	OR8AnP	6	11	137.68	FLVICVMVIELVFANLI	50	M	AC069561.10	51687 ... 50743
1046	OR1P1P	1	17	2.99	LLGDIALLTRLLLGVII	82	M	AF102538.1	139 ... 675
1047	OR7E12P	7	11	1.92	MAGGEFFSLHIMPAFGL	55	M	AF073989.1	547 ... 1515
1048	OR4A1P	4	11		LHGGVVGHFQVNGICV	57	M	AB030896.1	1 ... 906
1049	OR10G3	0	14	1.7	LHGSCGAHLQLTDIVVS	91	M	AF259072.1	19582 ... 18644
1050	OR10G1P	3	14	1.7	LHGSCGAHIQLTDIVAS	93	M	AF259072.1	55611 ... 54658
1051	OR10G2	0	14	1.7	LHGSCGAHIQLTDVVAS	91	M	AF259072.1	55611 ... 54658
1052	OR5Tn	0	11	51.94	MVGTCAAHIHAFVIEV	52	M	AF121977.1	262 ... 1197
1053	OR7EnP	8	3	136.02	MVACGVLDLHIIGSFGL	53	R	AF091580.1	7 ... 663
1054	OR7EnP	5	3	136.02	MAGGKFLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
1055	OR4AnP	2	11	50.93	LHAGVVGHVQFMNGICV	61	M	AB030895.1	1 ... 924
1056	OR4C1	1	11	50.93	LHGGIIGHVQFVNSMCL	66	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1057	OR1EnP	7	17	2.9MMMYTLIMGILI	80	M	AF073961.1	32 ... 649
1058	OR7KnP	11	14	5.99	MIGCNFIELYMMIGIFG	49	R	AF091580.1	7 ... 663
1059	OR4CnP	3	11	50.93	LHDGIEGHIQFVNSMCA	61	M	AF102522.1	40 ... 660
1060	OR1RnP	11	17	2.9	MVGISAVHLHLIEGVVA	44	R	M64377.1	1 ... 939
1061	OR5AUn	0	14	1.22	MAATCGANIHCLEFANLS	51	M	AC069559.8	85584 ... 84655
1062	OR4Cn	0	11	50.96	LHAGVVGHIQFVNSICI	69	M	AF102522.1	40 ... 660
1063	OR4Cn	0	11	50.96	VHGCIVGHVQLLSICV	57	M	AB030895.1	1 ... 924
1064	OR13Dn P	2	9	86.89	MLGSCWITLRLFTVIVL	58	M	AJ251154.1	2703 ... 1747
1065	OR5n				ASASLTSYVHNEEEVFV	44	M	AL359352.1	111313 ... 112242
1066	OR2Hn				LLGTCVMQVQSLSSLVV	83	M	AL078630.1	48786 ... 47851
1067	ORn				25	M	AC074177.4	88434 ... 88916
1068	ORn			EINLLLARGKAL	29	M	AF283814.1	1 ... 930
1069	ORn				NNNNNFXXSLHLCCCILI	29	M	AC074177.4	128803 ... 129726
1070	ORn				TLLLLTFQHHL.....	27	M	L14569.1	62 ... 667
1071	OR6Fn				..CCCWPIPTSAIAVIS	46	R	M64386.1	130 ... 975
1072	ORn			ILLLLL	33	R	U50947.1	418 ... 1350
1073	ORn				..CCCLIPFFFTSGYSW	24	R	M64392.1	1 ... 942
1074	OR10An				PLGECDPEEQMYVGLVM	51	M	AF247657.1	1 ... 945
1075	ORn				IPNASRRRRR....PP	25	R	M64388.1	1 ... 942
1076	OR2Ln				FLAGAGINAHYVSTFLF	51	M	AF102527.1	22 ... 669
1077	OR10Jn				LTGICGIMVQSNVSVLL	57	M	X92969.1	8035 ... 8961
1078	OR1Kn				LLLLLMVNLYLIKGVVT	50	R	M64377.1	1 ... 939
1079	OR10Dn				LHGSCGLHILLSNVISG	69	M	AC074177.4	12106 ... 13038
1080	ORn			CCCI	41	R	M64376.1	1 ... 999

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1081	OR2Ln				SLACGGLNAHFVRTLSF	52	M	AF102537.1	16 ... 669
1082	ORn				HHHHHRLESSSLLLLLL	38	M	AC073945.4	152209 ... 153150
1083	ORn			LLLLLS	27	M	AL365336.1	41087 ... 41711
1084	OR2n			GGGGGG	57	M	AF102521.1	22 ... 669

5 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that various changes and modifications can be practiced without departing from the spirit of the invention. Therefore the foregoing descriptions and examples should not be construed as limiting the scope of the invention.

10

 All patents, patent applications, and publications cited herein are hereby incorporated by reference in their entirety. In particular, the following documents are hereby incorporated by reference in their entirety: United States Provisional Patent Applications Serial Nos. 60/145,412, filed July 23, 1999; 60/155,126, filed September 22, 1999; 60/158,495, filed October 8, 1999; 60/158,615, filed October 8, 1999; 60/181,113, filed February 8, 2000; 60/181,115, filed February 8, 2000; 60/184,809, filed February 24, 2000; 60/188,332, filed March 9, 2000; and United States Patent Applications Serial Nos. 09/620,753, filed July 21, 2000; and 09/621,122, filed July 21, 2000.

CLAIMS

What is claimed is:

- 5 1. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence that is at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through
10 SEQ ID NO:152 and encoding a polypeptide having olfactory receptor function.
2. An expression vector comprising a polynucleotide sequence of claim 1.
3. A host cell comprising the expression vector of claim 2.
- 15 4. An isolated and purified olfactory receptor polypeptide comprising the translated sequence of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of the translated sequence of SEQ ID
20 NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152 and having olfactory receptor function.
5. A host cell expressing a polypeptide of claim 4 or a functional fragment thereof.
- 25 6. A phage expressing a polypeptide of claim 4 or a functional fragment thereof.
7. A preparation containing a polypeptide of claim 4, further comprising
30 biological or synthetic molecules which maintain the functional structure of the polypeptide.

8. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 or a nucleotide sequence having a sequence at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 and encoding a polypeptide having olfactory receptor function.
9. An expression vector comprising a polynucleotide sequence of claim 8.
10. A host cell comprising the expression vector of claim 9.
11. An isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function.
12. A host cell expressing a polypeptide of claim 11 or a functional fragment thereof.
13. A phage expressing a polypeptide of claim 11 or a functional fragment thereof.
14. A preparation containing a polypeptide of claim 11, further comprising biological or synthetic molecules which maintain the functional structure of the polypeptide.
15. A library of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

16. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 50 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through
5 SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

17. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 100 polynucleotides of SEQ ID NO:1 through
10 SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

18. A library of olfactory receptors according to claim 15, wherein the library
15 comprises the expression products of at least 200 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

19. A library of olfactory receptors according to claim 15, wherein the library
20 comprises the expression products of at least 500 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

20. A library of olfactory receptors suitable for determining the interaction
25 pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

21. A library of olfactory receptors according to claim 20, wherein the library
30 comprises at least 50 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,

wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

22. A library of olfactory receptors according to claim 20, wherein the library
5 comprises at least 100 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,
wherein said polypeptides are functional olfactory receptors; or functional fragments of
said polypeptides.

23. A library of olfactory receptors according to claim 20, wherein the library
10 comprises at least 200 polypeptides of SEQ ID NOS of SEQ ID NO: 1085 through SEQ
ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional
fragments of said polypeptides.

24. A library of olfactory receptors according to claim 20, wherein the library
15 comprises at least 500 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,
wherein said polypeptides are functional olfactory receptors; or functional fragments of
said polypeptides.

25. A method for determining the binding pattern of a composition with
20 olfactory receptors, comprising the steps of:
exposing the composition to a library according to claim 21; and
determining whether the composition binds to each olfactory receptor, thereby
determining the overall binding pattern of the composition.

26. The method of claim 25, wherein the composition consists essentially of one
25 compound or chemical.

27. The method of claim 25, wherein the composition comprises at least two
30 compounds or chemicals.

28. The method of claim 25, wherein the step of determining whether the
composition binds to each olfactory receptor further comprises a determination of the

approximate binding constant with which the composition binds to each receptor or functional fragment thereof.

29. The method of claim 25, further comprising the step of determining whether
5 a receptor or functional fragment thereof to which the composition binds is activated.

30. The method of claim 29, further comprising the step of determining the
absolute or relative amount by which the receptor or functional fragment thereof is
activated.

10

31. A DNA array or a DNA chip comprising DNA segments derived from SEQ ID
NO: 153 through SEQ ID NO: 1084.

32. A method of determining differences among individuals with respect to their
15 olfactory faculties, comprising the steps of comparing the olfactory DNA of the individual
against the array or chip of claim 31.

33. A method to determine single nucleotide polymorphisms in olfactory receptors,
comprising the steps of uniquely amplifying olfactory receptor sequences from DNA
20 obtained from one or more individuals, based on primers designed according to the first 25
bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through
SEQ ID NO: 1084, and determining the similarities and differences between said amplified
DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

cttggtcctt	ccacatgatt	gtgggtcacga	tgtactatgg	gccatttatt	tttacatata	780
tgagacctaa	atcataccac	actccaggcc	aggataagtt	cctggcaata	ttctatacga	840
tcctcacacc	cacactcaac	cctttcatct	acagcttttag	gaataaagat	gttctggcgg	900
tgatgaaaaa	tatgctcaaa	agtaactttc	tgcacaaaaa	aatgaatagg	aaaattcctg	960
aatgtgtgtt	ctgtctattt	ctatgtttaa	tgcctgaagg	atactcatga	gaggtttcct	1020

<210> 644

<211> 932

<212> DNA

<213> Unknown (H38g493 nucleotide)

<220>

<223> Synthetic construct

<400> 644

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gggaacgccc	tcctcatagg	gctgaacgtg	ctgcaccctc	gcctgcacaa	ccccatgtac	180
ttctcagcaa	cctctccctc	atggacatct	gcggcacctc	ctcctttgtg	cctctcatgc	240
tagacaattt	cctggaaacc	cagaggacca	tttccttccc	tggctgtgcc	ctgcagatgt	300
acctgacctt	ggcgctggga	tcaacggagt	gcctgctgct	ggctgtgatg	gcatatgacc	360
gttatgtggc	tatctgccag	ccgcttaggt	acccagagct	catgagtggg	cagacctgca	420
tgcagatggc	agcgctgagc	tgggggacag	gctttgccaa	ctcactgcta	cagtccatcc	480
ttgtctggca	cctccccctc	tgtggccacg	tcatacaacta	cttctatgag	atcttggcag	540
tgctaaaact	ggcctgtggg	gacatctccc	tcaatgcgct	ggcattaatg	gtggccacag	600
ccgtcctgac	actggccccc	ctcttgctca	tctgcctgtc	ttaccttttc	atcctgtctg	660
ccatccttag	ggtacctctt	gctgcaggcc	ggtgcaaagc	cttctccacc	tgctcagccc	720
accgcacagt	ggtggtggtt	ttttatggga	caatctcctt	catgtacttc	aaacccaagg	780
ccaaggatcc	caacgtggat	aagactgtcg	cattgtttcta	cggggttgtg	acgccctcgc	840
tgaaccccat	catttacagc	ctgaggaatg	cagaggtgaa	agctgccgtc	ctaactctgc	900
tgagaggagg	tttgcctctc	aggaaagcat	cc			932

<210> 645

<211> 957

<212> DNA

<213> Unknown (H38g494 nucleotide)

<220>

<223> Synthetic construct

<400> 645

atgatggaaa	tagccaatgt	gagttctcca	gaagtctttg	tcctcctggg	cttctccaca	60
cgaccctcac	tagaaactgt	cctcttcata	gttgtcttga	gtttttacat	ggtatcgatc	120
ttggggcaatg	gcatcatcat	tctgggtctc	catacagatg	tgcacctcca	cacacctatg	180
tacttctttc	ttgccaaact	ccccttctctg	gacatgagct	tcaccacgag	cattgtccca	240
cagctcctgg	ctaacctctg	gggaccacag	aaaaccataa	gctatggagg	gtgtgtggtc	300
cagttctata	tctcccattg	gctgggggca	accgagtgtg	tcctgctggc	caccatgtcc	360
tatgaccgct	acgctgccat	ctgcaggcca	ctccattaca	ctgtcattat	gcatccacag	420
ctttgccttg	ggctagcttt	ggcctcctgg	ctgggggggtc	tgaccaccag	catggtgggc	480
tccacgetca	ccatgctcct	accgctgtgt	gggaacaatt	gcatcgacca	cttcttttgc	540
gagatgcccc	tcattatgca	actggcttgt	gtggatacca	gcctcaatga	gatggagatg	600
tacctggcca	gctttgtctt	tgttgtcctg	cctctggggc	tcatectggt	ctcttacggc	660
cacattgccc	gggcctgtgt	gaagatcagg	tcagcagaag	ggcggagaaa	ggcattcaac	720
acctgttctt	cccacgtggc	tgttgtgtct	ctgttttacg	ggagcatcat	cttcatgtat	780
ctccagccag	ccaagagcac	ctcccatgag	cagggcaagt	tcatagctct	gttctacacc	840
gtagtcactc	ctgcgctgaa	cccacttatt	tacacctga	ggaacacgga	ggtgaagagc	900
gccctccggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

<210> 646

<211> 792

<212> DNA

<213> Unknown (H38g495 nucleotide)

<220>

<223> Synthetic construct

<400> 646

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attcactggg	accacgggtt	ccacacgccc	atgtacttcc	tcctgagcca	actttccctc	120
atggacgtga	tgctggtttc	caccactgtg	cccaaaatgg	cggttgacta	cttgaccgga	180
agtaaggcca	tctcccgcgc	tggtgtgggt	gcgcagatct	tcttctctcc	cacactgggt	240
ggtggagagt	gcttctctct	agcagccatg	gcctatgacc	gctatgcggc	tgtctgccac	300
ccactccgat	atcccaactct	catgagctgg	cagctgtgcc	tgaggatgaa	cctgtcgtgt	360
tggtcctcgg	gtgcagctga	cgggctcctg	caggctgttg	ctaccctgag	cttcccatat	420
tgcgggtgac	acgagatcga	tcacttcttc	tgcgagaccc	ccgtgctggt	gcgtttggct	480
tgtgctgaca	cttcagtctt	cgaaaacgcc	atgtacatct	gctgtgtgtt	aatgctcctg	540
gtccccctttt	ccctcatcct	gtcctcctat	ggctctatcc	tcgctgctgt	tctgcacatg	600
cgctctacag	aagcccgcga	gaaggccttt	gccacctgct	cttcacatgt	ggctgtgggt	660
ggactctttt	atggagctgc	cattttttacc	tatatgagac	ccaaatccca	caggctccact	720
aaccacgaca	aggttgtgtc	agccttctat	actatgttca	cccctttact	aaacccctc	780
atctacagt	tg					792

<210> 647

<211> 662

<212> DNA

<213> Unknown (H38g496 nucleotide)

<220>

<223> Synthetic construct

<400> 647

aatctgtctt	tcttagatct	ctgctttaca	gcaagcattg	cccctcagct	gctgtggaac	60
ctgggggggtc	cagagaagac	catcacctac	cacggctgtg	tggcccaact	ctacatctac	120
atgatgctgg	gtccaccga	gtgcgtctc	ctggttgtca	tgtcccatga	ccgctatgtg	180
gccgtctgcc	ggctccctgca	ctacatggca	gtcatgcgcc	cacatctctg	cctgcagctg	240
gtgactgtgg	cctgggtgctg	tggtctccta	aactccttca	tcattgtgtc	tcagacgatg	300
cagctctccc	ggtgtggacg	tcgcagggtg	gaccacttcc	tgtgtgagat	gcctgctctt	360
attgccatgt	cttgtgagga	aaccatgctg	gtagaagcga	ttcacctttg	ccctgggggt	420
ggctctcctc	ctgggtgccg	tctccctcat	cctcatctcc	tacggcgtga	ttgcagccgc	480
ggtgctgagg	atgaagtcag	cagcagggcg	aaagaaagcc	ttccacacct	gctcttctca	540
cctcacagt	gtctctctct	<u>tctacggaac</u>	catcatctac	ggtgtacctg	aagccggcca	600
acagctactc	ccaagatcag	gggaagtcc	tgactctctt	ctacaccatc	gtcattccca	660
gc						662

<210> 648

<211> 936

<212> DNA

<213> Unknown (H38g497 nucleotide)

<220>

<223> Synthetic construct

<400> 648

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ccagccctgg	agcatctgct	cttccctctg	tgtcagcca	tgtacctggt	gacctctctg	120
gggaacacag	ccatcatggc	ggtgagcgtg	ctagatatcc	acctgcacac	gcccgtgtac	180
ttcttctctg	gcaacctctc	tacctgggac	atctgctaca	cgcccacctt	tgtgcctctg	240
atgctggtcc	acctctctgt	atcccggaag	accatctcct	ttgctgtctg	tgccatccag	300
atgtgtctga	gcctgtccac	gggtccacg	gagtgcctgc	tactggccat	cacggcctat	360
gaccgctacc	tggccatctg	ccagccactc	aggtaccacg	tgctcatgag	ccaccggctc	420
tgcgtgctgc	tgatgggagc	tgctgggtc	ctctgcctcc	tcaagtccgt	gactgagatg	480
gtcatctcca	tgaggctgcc	cttctgtggc	caccacgtgg	tcagtcactt	cacctgcaag	540

atcctggcag	tgctgaagct	ggcatgcggc	aacacgtcgg	tcagcgaaga	cttcctgctg	600
gcgggctcca	tcctgctgct	gcctgtaccc	ctggcattca	tctgcctgtc	ctacttgctc	660
atcctggcca	ccatcctgag	ggtgccctcg	gocgccaggt	gctgcaaage	cttctccacc	720
tgcttggcac	acctggctgt	agtgtgtctt	ttctacggca	ccatcatctt	catgtacttg	780
aagcccaaga	gtaaggaagc	ccacatctct	gatgaggtct	tcacagtcct	ctatgccatg	840
gtcacgacca	tgctgaaccc	caccatctac	agcctgagga	acaaggaggt	gaaggaggcc	900
gccaggaagg	tgtggggcag	gagtcggggc	tccagg			936

<210> 649

<211> 940

<212> DNA

<213> Unknown (H38g498 nucleotide)

<220>

<223> Synthetic construct

<400> 649

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gaaacaccct	tattattatc	ctgattcttg	tggattacag	gctccactca	cccatgtatt	180
tcttcctcag	caatctctct	ttcagtgaag	cattaaccat	aacctgtgct	gttcctaaga	240
tgctggaggg	cttcccgtag	gaaaggaaga	gcatacacaag	tggcgaatgc	tctgcacagt	300
cctattttcta	ttttctttcc	ggatgcactg	agttttattcc	ttttgctgtc	atgtcctatg	360
accgctatgt	ggccatttgc	agtcctcttc	agtaccctgc	aattatgacc	agctcactct	420
gtgcccacct	cgtcatectc	tcctgggtgg	gtggctttct	cctcatgctc	ccatccacca	480
tcctcaaggc	aggactgcca	cactgtgggc	ccaacgtgat	tgagcacttt	ttctgtgaca	540
gcgcccctct	cctccacctg	gcctgtgctg	acattcgtgc	tattgagctg	ttggactttc	600
tcagctcact	ggtcctgate	ctcagctccc	tctcactcac	agtgggtctcc	tatgtttaca	660
tcattctccac	cattctgaag	ataccctcag	gccaaaggtca	acgcaaagcc	tttgccacct	720
gtgcctctca	cttcacggag	gtctccgtag	gctatgggat	ctccatcttt	gtctatgttc	780
acccctcaca	gaagagcagc	ctgcacctca	acaagatcct	ctttatcctc	tccagcatca	840
tcacaccctc	cctgaatccc	ttcgtcttca	gtctgtggaa	tgaacccatg	aaagatgcac	900
tgaaggacgc	ctcggccgga	ggacagagct	tgctcaaagg			940

<210> 650

<211> 927

<212> DNA

<213> Unknown (H38g499 nucleotide)

<220>

<223> Synthetic construct

<400> 650

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atgtgcattt	tgcattcgat	tctcttcttg	ttgatttatt	tgtgtgccct	gatggggaat	120
gtcctcatta	tcatgatcac	aactttggac	catcatctcc	acacccccgt	gtattttcttc	180
ttgaagaate	tatctttctt	ggatctctgc	cttatttcag	tcacggctcc	caaattctatc	240
gccaattctt	tgatacacaa	caactccatt	tcattccttg	gctgtgtttc	ccagggtcttt	300
ttgttgcttt	cttcagcate	tgcagagctg	ctcctcctca	cggtagatgc	ctttgaccgc	360
tatactgcta	tatgtcacc	tctgcactat	gatgtcatca	tggacaggag	cacctgtgtc	420
caaagagcca	ctgtgtcttg	gctgtatggg	ggtctgattg	ctgtgatgca	cacagctggc	480
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cagttattag	ctattttctg	ctcagaaaaat	ttaataagag	aaattgcact	catccttatt	600
aatgtagttt	tggattttctg	ctgtttttatt	gtcatcatca	ttacctatgt	ccacgtcttc	660
tctacagtca	agaagatccc	ttccaagaaa	ggccagtcac	aagcctactc	tatttgccct	720
ccacacttgc	tggttgtgtt	atttctttcc	actggattca	ttgcttatct	gaagccagct	780
tcagagtctc	cttctatatt	ggatgctgta	atttctgtgt	tctacactat	gctgccccca	840
acctttaate	ccattatata	cagtttgaga	aacaaggcca	ttaagggtggc	tctgggggatg	900
ttgataaagg	gaaagctcac	caaaaaag				927

<210> 651

Tyr Ala Gln Lys Xaa Leu Ser Ala Gln Lys Asn Glu Xaa Glu Asn Ser
 305 310 315 320
 Xaa Met Cys Val Leu Ser Ile Ser Met Leu Asn Ala Xaa Arg Ile Leu
 325 330 335
 Met Arg Trp Phe Pro
 340

<210> 1576
 <211> 311
 <212> PRT
 <213> Unknown (H38g493 protein)

<220>
 <223> Synthetic construct

<400> 1576
 Met Lys Trp Ala Asn Gln Thr Ala Val Thr Glu Tyr Val Leu Met Gly
 1 5 10 15
 Leu His Glu His Cys Asn Leu Glu Val Val Leu Phe Val Phe Cys Leu
 20 25 30
 Gly Ile Tyr Ser Val Asn Val Leu Gly Asn Ala Leu Leu Ile Gly Leu
 35 40 45
 Asn Val Leu His Pro Arg Leu His Asn Pro Met Tyr Phe Phe Ser Asn
 50 55 60
 Leu Ser Leu Met Asp Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Met
 65 70 75 80
 Leu Asp Asn Phe Leu Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys
 85 90 95
 Ala Leu Gln Met Tyr Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu
 100 105 110
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro
 115 120 125
 Leu Arg Tyr Pro Glu Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala
 130 135 140
 Ala Leu Ser Trp Gly Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile
 145 150 155 160
 Leu Val Trp His Leu Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr
 165 170 175
 Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn
 180 185 190
 Ala Leu Ala Leu Met Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu
 195 200 205
 Leu Leu Ile Cys Leu Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg
 210 215 220
 Val Pro Ser Ala Ala Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala
 225 230 235 240
 His Arg Thr Val Val Val Phe Tyr Gly Thr Ile Ser Phe Met Tyr
 245 250 255
 Phe Lys Pro Lys Ala Lys Asp Pro Asn Val Asp Lys Thr Val Ala Leu
 260 265 270
 Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Ile Ile Tyr Ser Leu
 275 280 285
 Arg Asn Ala Glu Val Lys Ala Ala Val Leu Thr Leu Leu Arg Gly Gly
 290 295 300
 Leu Leu Ser Arg Lys Ala Ser,
 305 310

<210> 1577
 <211> 319
 <212> PRT
 <213> Unknown (H38g494 protein)

2

2

<220>

<223> Synthetic construct

<400> 1577

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Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
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Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
      20           25           30
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
      35           40           45
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
      65           70           75           80
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
      85           90           95
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
      100          105          110
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
      115          120          125
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
      130          135          140
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
      145          150          155          160
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
      165          170          175
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
      180          185          190
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
      195          200          205
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
      210          215          220
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
      225          230          235          240
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
      245          250          255
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
      260          265          270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
      275          280          285
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
      290          295          300
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
      305          310          315

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<210> 1578

<211> 264

<212> PRT

<213> Unknown (H38g495 protein)

<220>

<223> Synthetic construct

<400> 1578

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Met Met Val Leu Ser Ile Val Leu Thr Ser Leu Phe Gly Asn Ser Leu
 1           5           10           15
Met Ile Leu Leu Ile His Trp Asp His Arg Phe His Thr Pro Met Tyr
      20           25           30
Phe Leu Leu Ser Gln Leu Ser Leu Met Asp Val Met Leu Val Ser Thr
      35           40           45

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Thr Val Pro Lys Met Ala Ala Asp Tyr Leu Thr Gly Ser Lys Ala Ile
  50          55          60
Ser Arg Ala Gly Cys Gly Ala Gln Ile Phe Phe Leu Pro Thr Leu Gly
  65          70          75          80
Gly Gly Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala
          85          90          95
Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu
          100          105          110
Cys Leu Arg Met Asn Leu Ser Cys Trp Leu Leu Gly Ala Ala Asp Gly
          115          120          125
Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His
          130          135          140
Glu Ile Asp His Phe Phe Cys Glu Thr Pro Val Leu Val Arg Leu Ala
          145          150          155          160
Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val
          165          170          175
Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu
          180          185          190
Ile Leu Ala Val Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys
          195          200          205
Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe Tyr
          210          215          220
Gly Ala Ala Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr
          225          230          235          240
Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro Leu
          245          250          255
Leu Asn Pro Leu Ile Tyr Ser Val
          260

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<210> 1579

<211> 220

<212> PRT

<213> Unknown (H38g496 protein)

<220>

<223> Synthetic construct

<400> 1579

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Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
  1          5          10          15
Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
          20          25          30
Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
          35          40          45
Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
          50          55          60
Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
          65          70          75          80
Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
          85          90          95
Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
          100          105          110
Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
          115          120          125
Met Leu Val Glu Ala Ile Thr Phe Ala Leu Gly Val Ala Leu Leu Leu
          130          135          140
Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr Gly Val Ile Ala Ala Ala
          145          150          155          160
Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
          165          170          175
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile

```


	180		185		190
Tyr Val Tyr	Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp	Gln Gly Lys			
	195		200		205
Phe Leu Thr	Leu Phe Tyr Thr Ile Val Ile Pro Ser				
	210		215		220

<210> 1580
 <211> 312
 <212> PRT
 <213> Unknown (H38g497 protein)

<220>
 <223> Synthetic construct

<400> 1580

Met Glu Pro	Leu Asn Arg Thr Glu Val Ser Glu Phe Phe Leu Lys Gly	
1	5	10 15
Phe Ser Gly Tyr	Pro Ala Leu Glu His Leu Leu Phe Pro Leu Cys Ser	
	20	25 30
Ala Met Tyr	Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Met Ala Val	
	35	40 45
Ser Val Leu	Asp Ile His Leu His Thr Pro Val Tyr Phe Phe Leu Gly	
	50	55 60
Asn Leu Ser	Thr Leu Asp Ile Cys Tyr Thr Pro Thr Phe Val Pro Leu	
65	70	75 80
Met Leu Val	His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Ala Val	
	85	90 95
Cys Ala Ile	Gln Met Cys Leu Ser Leu Ser Thr Gly Ser Thr Glu Cys	
	100	105 110
Leu Leu Leu	Ala Ile Thr Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln	
	115	120 125
Pro Leu Arg	Tyr His Val Leu Met Ser His Arg Leu Cys Val Leu Leu	
	130	135 140
Met Gly Ala	Ala Trp Val Leu Cys Leu Leu Lys Ser Val Thr Glu Met	
145	150	155 160
Val Ile Ser	Met Arg Leu Pro Phe Cys Gly His His Val Val Ser His	
	165	170 175
Phe Thr Cys	Lys Ile Leu Ala Val Leu Lys Leu Ala Cys Gly Asn Thr	
	180	185 190
Ser Val Ser	Glu Asp Phe Leu Leu Ala Gly Ser Ile Leu Leu Leu Pro	
	195	200 205
Val Pro Leu	Ala Phe Ile Cys Leu Ser Tyr Leu Leu Ile Leu Ala Thr	
	210	215 220
Ile Leu Arg	Val Pro Ser Ala Ala Arg Cys Cys Lys Ala Phe Ser Thr	
225	230	235 240
Cys Leu Ala	His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Ile	
	245	250 255
Phe Met Tyr	Leu Lys Pro Lys Ser Lys Glu Ala His Ile Ser Asp Glu	
	260	265 270
Val Phe Thr	Val Leu Tyr Ala Met Val Thr Thr Met Leu Asn Pro Thr	
	275	280 285
Ile Tyr Ser	Leu Arg Asn Lys Glu Val Lys Glu Ala Ala Arg Lys Val	
	290	295 300
Trp Gly Arg	Ser Arg Ala Ser Arg	
305	310	

<210> 1581
 <211> 314
 <212> PRT
 <213> Unknown (H38g498 protein)
